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106866

From: Li, Ruixiang
Sent: Monday, October 27, 2003 5:12 PM
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Subject: Sequence search of Application NO:10/070,241

Please do a standard search on

- (i) SEQ ID NO: 2 against commercial nucleic acid databases;
- (ii) SEQ ID NO: 1 against commercial amino acid databases.

Thank you very much!

Ruixiang Li
GAU 1646
CM1 10E18
Mail Box 10D19
306-0282

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: 10/28/03
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Online time: _____

TYPE OF SEARCH: /
NA Sequences: _____
AA Sequences: / _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: 01/02
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

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RESULT 6
US-10-272-983-37
; Sequence 37, Application US/10272983
; Publication No. US20030148450A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Dang, Huang T.
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
; FILE REFERENCE: AREN0050
; CURRENT APPLICATION NUMBER: US/10/272,983
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: US/09/417,044
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 60/109,213
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,851
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/123,946
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,949
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/136,436
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,437
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,439
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,567
; PRIOR FILING DATE: 1999-05-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 37
; LENGTH: 1296
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-272-983-37

Query Match      53.6%; Score 1294.4; DB 12; Length 1296;
Best Local Similarity 99.9%; Pred. No. 2.9e-285;
Matches 1295; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 354 ATGCAGGCGCTTAACATTACCCCGGAGCAGTCTCTCGGCTGCTGGGACCAACACCTG 413
DB 1 ATGCAGGCGCTTAACATTACCCCGGAGCAGTCTCTCGGCTGCTGGGACCAACACCTG 60

QY 414 ACGCGGAGCAGTTCATCGCTCTGTACCGGCTGCGACCGCTCTGTACACCCCGAGAGCTG 473
DB 61 ACGCGGAGCAGTTCATCGCTCTGTACCGGCTGCGACCGCTCTGTACACCCCGAGAGCTG 120

QY 474 CCGGACGCGCAAGCTGCTGTCTACCGGCTGCTCATCTTCCCTCTGGCGCTC 533
DB 121 CCGGACGCGCAAGCTGCTGTCTACCGGCTGCTCATCTTCCCTCTGGCGCTC 180

QY 534 TTGGCAATGCTCTGGTGTCTACGTGTGTACCGCGGAGCCATGGCACCCCTCACC 593
DB 131 TTGGCAATGCTCTGGTGTCTACGTGTGTACCGCGGAGCCATGGCACCCCTCACC 240

QY 594 AACATCTTTATCTGCTCTTGGCGCTCAGTGACCTGCTCATCACCTTCTTGTGCAATTC 653
DB 241 AACATCTTTATCTGCTCTTGGCGCTCAGTGACCTGCTCATCACCTTCTTGTGCAATTC 300

QY 654 GTCACCATGCTCCAGAACATTTCCGACAACTGGCTGGGGGGTCTTTTCATTTGCAAGATG 713
DB 301 GTCACCATGCTCCAGAACATTTCCGACAACTGGCTGGGGGGTCTTTTCATTTGCAAGATG 360

QY 714 GTGCCATTGTCCAGTCTACCGCTGTGTGACAGAAATCCTCACTATGACCTGCAATGCT 773
DB 714 GTGCCATTGTCCAGTCTACCGCTGTGTGACAGAAATCCTCACTATGACCTGCAATGCT 773
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RESULT 7

US-10-393-807-37

; Sequence 37, Application US/10393807

; Publication No. US20030175891A1

; GENERAL INFORMATION:

; APPLICANT: Chen, Ruoping

; APPLICANT: Dang, Huang T.

; APPLICANT: Liaw, Chen W.

; APPLICANT: Lin, I-Lin

; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors

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DB 361 GTGCCATTGTCCAGTCTACCCCTGTTGTGACAGAAATGCTCACTATGACCTGCTCATGTGCT 420
QY 774 GTGGAAGGCACACAGGAGCTTGTGCATCTCTTTTAAATGAAGTGGCAATACACCAACCGA 833
DB 421 GTGGAAGGCACACAGGAGCTTGTGCATCTCTTTTAAATGAAGTGGCAATACACCAACCGA 480
QY 834 AGGGCTTTTCACAAATGCTAGGTGTGTCTGGCTGGTGGGAGTGTATGAGTATGAGTATGAGT 893
DB 481 AGGGCTTTTCACAAATGCTAGGTGTGTCTGGCTGGTGGGAGTGTATGAGTATGAGTATGAGT 540
QY 894 TGGCAGCTGCAACAACTTGGAGATCAATATGACTTCTTATATGAAAGGAAACACATCTGTC 953
DB 541 TGGCAGCTGCAACAACTTGGAGATCAATATGACTTCTTATATGAAAGGAAACACATCTGTC 600
QY 954 TGCCTTAGAAGAGTGGACAGCCCTGTGCACCAAGAGATCTACACCACTTCACTTCTGTC 1013
DB 601 TGCCTTAGAAGAGTGGACAGCCCTGTGCACCAAGAGATCTACACCACTTCACTTCTGTC 660
QY 1014 ATCCCTCTTCTCTGCTCTTATGAGTGTGTCTTATGAGTGTGTCTTATGAGTGTGTGTATGAA 1073
DB 661 ATCCCTCTTCTCTGCTCTTATGAGTGTGTCTTATGAGTGTGTCTTATGAGTGTGTATGAA 720
QY 1074 CTTTGGATAAAGAAAGAGTTGGGGATGTTTCAGTGTCTTGAATCTTATTCATGAAAGAA 1133
DB 721 CTTTGGATAAAGAAAGAGTTGGGGATGTTTCAGTGTCTTGAATCTTATTCATGAAAGAA 780
QY 1134 ATGTCACAAATAGCCAGGAAGAAAGAGTGTGTATGATGATGATGATGATGATGATGATGATGAT 1193
DB 781 ATGTCACAAATAGCCAGGAAGAAAGAGTGTGTATGATGATGATGATGATGATGATGATGATGAT 840
QY 1194 CTCCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1253
DB 841 CTCCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 900
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DB 901 TTTGAAAAGGAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960
QY 1314 GGATTTTCCAACTCCATCTGTAAATCCCAATGCTATGATGATGATGATGATGATGATGATGATGAT 1373
DB 961 GGATTTTCCAACTCCATCTGTAAATCCCAATGCTATGATGATGATGATGATGATGATGATGATGAT 1020
QY 1374 AAAATGTTTTGTCTGTCAGTTTGTATTGTCATGATGATGATGATGATGATGATGATGATGATGAT 1433
DB 1021 AAAATGTTTTGTCTGTCAGTTTGTATTGTCATGATGATGATGATGATGATGATGATGATGATGAT 1080
QY 1434 AGGCATGGAATTTACGAAATTTACAAATGATGCGGAAGAAAGCAAAAGTTTTTCCCTCAGAGAG 1493
DB 1081 AGGCATGGAATTTACGAAATTTACAAATGATGCGGAAGAAAGCAAAAGTTTTTCCCTCAGAGAG 1140
QY 1494 AATCCAGTGGAGGAAACCAAGAGGAGAGCAATTCAGTGTGATGCGCAATTCAGTGTGATGATGAT 1553
DB 1141 AATCCAGTGGAGGAAACCAAGAGGAGAGCAATTCAGTGTGATGCGCAATTCAGTGTGATGATGAT 1200
QY 1554 TGTGAACAGACAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1613
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QY 1614 CTGGCTGAGAAATTCCTTTTAGACAGAGTGGGCAATTA 1649
DB 1261 CTGGCTGAGAAATTCCTTTTAGACAGAGTGGGCAATTA 1296
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Query Match	53.6%	Score 1294.4	DB 12	Length 1296
Best Local Similarity	99.9%	Pred. No. 2.9e-285		
Matches 1295	Conservative 0	Mismatches 1	Indels 0	Gaps 0
QY	354	ATCAGGCGTTTAACTTACCCGGAGCAGTTCTCGGCTGCTCGGGACCAACCTG	413	
Db	1	ATCAGGCGTTTAACTTACCCGGAGAGTTCTCGGCTGCTCGGGACCAACCTG	60	
QY	414	ACCGGGAGCAGTTCAFCGCTCTGTACCGGCTGCGACCGCTCGTCTACACCCACAGAGCTG	473	
Db	61	ACCGGGAGCAGTTCAFCGCTCTGTACCGGCTGCGACCGCTCGTCTACACCCACAGAGCTG	120	
QY	474	CCGGGACGCGCAAGCTGGCCCTCGTGTCTACCGGCTGCTCATCTTCGCCCTGGCGCTC	533	
Db	121	CCGGGACGCGCAAGCTGGCCCTCGTGTCTACCGGCTGCTCATCTTCGCCCTGGCGCTC	180	
QY	534	TTTGGCAATGCTCTGGGTGTTCTACGTGGTGACCCGCGACGAAGGCATGCGCACCGTCACC	593	
Db	181	TTTGGCAATGCTCTGGGTGTTCTACGTGGTGACCCGCGACGAAGGCATGCGCACCGTCACC	240	
QY	594	AACATCTTTATCTGCTCCTTGGGCGCTCAGTGA	653	
Db	241	AACATCTTTATCTGCTCCTTGGGCGCTCAGTGA	300	
QY	654	GTCAACATGCTCCAGAACATTTCCGCAACCTGGCTGGGGGGTCTTTCATTTGCAAGTG	713	
Db	301	GTCAACATGCTCCAGAACATTTCCGCAACCTGGCTGGGGGGTCTTTCATTTGCAAGTG	360	
QY	714	GTGCCATTTGTCCAGTCTACCGCTGTTGTGACAGAAATCCCTCACTATGACTGCATTTGCT	773	
Db	361	GTGCCATTTGTCCAGTCTACCGCTGTTGTGACAGAAATGCTCACTATGACTGCATTTGCT	420	
QY	774	GTGGAAGGCACCGAGGACTTTGTCATCTCTTTTAAATGAAGTGGCAATACACCAACCGA	833	
Db	421	GTGGAAGGCACCGAGGACTTTGTCATCTCTTTTAAATGAAGTGGCAATACACCAACCGA	480	
QY	834	AGGGCTTTCACAATGCTAGTGTGGTCTGGCTGGTGGCAGTCATCTGTAGGATCACCCATG	893	
Db	481	AGGGCTTTCACAATGCTAGTGTGGTCTGGCTGGTGGCAGTCATCTGTAGGATCACCCATG	540	
QY	894	TGGCAGTGCACCAACTTGGATCAAAATATGACTTCTCTATATGAAAGGAAACATCTGCG	953	

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RESULT 8
US/10-225-567A-509
Sequence 509, Application US/10225567A
Publication No. US20030113798A1
GENERAL INFORMATION:
APPLICANT: LifeSpan Biosciences
APPLICANT: Brown, Joseph P.
APPELLANT: Burner, Glenna C.
APPLICANT: Rough, Christine L.
TITLE OF INVENTION: ANTIGENIC PEPTIDES
FILE REFERENCE: 1970-4-4
CURRENT APPLICATION NUMBER: US/10/225
CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/257,144
PRIOR FILING DATE: 2000-12-19
NUMBER OF SEQ IDS NOS: 2292
SOFTWARE: Patent version 3.1
SEQ ID NO 509
LENGTH: 1368
TYPE: DNA
ORGANISM: Homo sapiens

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QY 241 LWIKRVDGSLRTIHGKMSKIARKKRAVIMMVTVALFAVCWAPFHVHMMIEYSN 300
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 QY 301 FEKEYDDVTIKMFAIVQIIGFNSICNPVYAFMNFKNVLSAVCYCIVNKTSPAQ 360
 Db 301 FEKEYDDVTIKMFAIVQIIGFNSICNPVYAFMNFKNVLSAVCYCIVNKTSPAQ 360
 QY 361 RHNSGITMWRKAKFSLRENPEETKGEAFSDGNIEVKLCBOTEEKKLRHLALFRSE 420
 Db 361 RHNSGITMWRKAKFSLRENPEETKGEAFSDGNIEVKLCBOTEEKKLRHLALFRSE 420
 QY 421 LAENSPDLSGH 431
 Db 421 LAENSPDLSGH 431

RESULT 6
 US-10-080-263C-2
 ; Sequence 2, Application US/10080263C
 ; Publication No. US20030143670A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bonini, James A.
 ; APPLICANT: Huang, Ling-Yan
 ; APPLICANT: Wilson, Amy
 ; TITLE OF INVENTION: DNA ENCODING SNORF44 RECEPTOR
 ; FILE REFERENCE: 1795/59370-A/JPW/ADM/ANX
 ; CURRENT APPLICATION NUMBER: US/10/080,263C
 ; CURRENT FILING DATE: 2002-02-20
 ; NUMBER OF SEQ ID NOS: 33
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 1
 ; LENGTH: 415
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-080-263C-2

Query Match 95.5%; Score 2135; DB 12; Length 415;
 Best Local Similarity 96.3%; Pred. No. 2e-185;
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 Db 1 MQALNITPEQFSRLRDHNLTRQFIATYRLRLPVVTPPELPGRAKLALVLTGVLIIFALAL 44
 QY 61 FGNALVFYVTRSKAMRTVTNIFICSLSALSDLLITFCIPVTMLQNSDNWLGGAFCIKM 120
 Db 45 FGNALVFYVTRSKAMRTVTNIFICSLSALSDLLITFCIPVTMLQNSDNWLGGAFCIKM 104
 QY 121 VPFVOSTAVVTEILMTCTIAVERHOGVHPFKMKQYTNRRAFMLGVVWLVAIVGSPM 180
 Db 105 VPFVOSTAVVTEILMTCTIAVERHOGVHPFKMKQYTNRRAFMLGVVWLVAIVGSPM 164
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 Db 165 WHVQOLEIKYDFLYEKEHICCLLEWTSVPHQKIYTTFFILVILPLLMWMLILYSKIGYE 224
 QY 241 LMKRVDGSLRTIHGKMSKIARKKRAVIMMVTVALFAVCWAPFHVHMMIEYSN 300
 Db 225 LMKRVDGSLRTIHGKMSKIARKKRAVIMMVTVALFAVCWAPFHVHMMIEYSN 284
 QY 301 FEKEYDDVTIKMFAIVQIIGFNSICNPVYAFMNFKNVLSAVCYCIVNKTSPAQ 360
 Db 285 FEKEYDDVTIKMFAIVQIIGFNSICNPVYAFMNFKNVLSAVCYCIVNKTSPAQ 344
 QY 361 RHNSGITMWRKAKFSLRENPEETKGEAFSDGNIEVKLCBOTEEKKLRHLALFRSE 420
 Db 345 RHNSGITMWRKAKFSLRENPEETKGEAFSDGNIEVKLCBOTEEKKLRHLALFRSE 404
 QY 421 LAENSPDLSGH 431
 Db 405 LAENSPDLSGH 415

RESULT 7
 US-09-990-940-16
 ; Sequence 16, Application US/09990940
 ; Publication No. US20030027252A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Tian, Hui
 ; APPLICANT: Zhao, Jiagang
 ; APPLICANT: Chen, Jin-Long
 ; APPLICANT: Cutler, Gene
 ; APPLICANT: An, Songzhu
 ; APPLICANT: Dai, Kang
 ; APPLICANT: Gupte, Jamila S.
 ; APPLICANT: Tulazik Inc.
 ; TITLE OF INVENTION: NO. US20030027252A1e1 Receptors
 ; FILE REFERENCE: 018781-007410US
 ; CURRENT APPLICATION NUMBER: US/09/990,940
 ; CURRENT FILING DATE: 2001-11-21
 ; PRIOR APPLICATION NUMBER: US 60/252,841
 ; PRIOR FILING DATE: 2000-11-22
 ; PRIOR APPLICATION NUMBER: US 60/257,636
 ; PRIOR FILING DATE: 2000-12-22
 ; PRIOR APPLICATION NUMBER: US 60/261,377
 ; PRIOR FILING DATE: 2001-01-12
 ; PRIOR APPLICATION NUMBER: US 60/279,554
 ; PRIOR FILING DATE: 2001-03-28
 ; PRIOR APPLICATION NUMBER: US 60/280,696
 ; PRIOR FILING DATE: 2001-03-29
 ; NUMBER OF SEQ ID NOS: 54
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 16
 ; LENGTH: 433
 ; TYPE: PRT
 ; ORGANISM: Mus sp.
 ; FEATURE:
 ; OTHER INFORMATION: mouse G-protein coupled receptor (GPCR) TGR346a
 US-09-990-940-16

Query Match 85.6%; Score 1944; DB 11; Length 433;
 Best Local Similarity 83.5%; Pred. No. 0.4e-165;
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 Db 61 FGNALVFYVTRSKAMRTVTNIFICSLSALSDLLITFCIPVTMLQNSDNWLGGAFCIKM 120
 QY 121 VPFVOSTAVVTEILMTCTIAVERHOGVHPFKMKQYTNRRAFMLGVVWLVAIVGSPM 180
 Db 121 VPFVOSTAVVTEILMTCTIAVERHOGVHPFKMKQYTNRRAFMLGVVWLVAIVGSPM 180
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 Db 301 FEKEYDDVTIKMFAIVQIIGFNSICNPVYAFMNFKNVLSAVCYCIVNKTSPAQ 360
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 QY 421 LAENSPDLSGH 431
 Db 421 LAENSPDLSGH 431

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 28, 2003, 10:08:35 ; Search time 86 seconds
(without alignments)
795.479 Million cell updates/sec

Title: US-10-070-241B-1

Perfect score: 2235

Sequence: 1 MQALNTPQFGRLLRDHNL.....RHLAIFRSLAENSLDSGH 431

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	2235	100.0	431	21	AAV94993 Human secreted pro
2	2235	100.0	431	22	ARG64289 Human GTP-binding
3	2235	100.0	431	22	AAE74773 Human G protein-co
4	2235	100.0	431	22	AAE48963 Human G protein-co
5	2235	100.0	431	23	AAU97735 Human TGR346 polyp
6	2235	100.0	431	23	AAU97735 Human neuropeptide
7	2235	100.0	431	24	ARG73503 Human G protein co
8	2232	99.9	431	21	AAV71309 Human orphan G pro
9	2232	99.9	431	21	AAAB02843 Human G protein co

10	2226	99.6	431	21	AAAB02853 Human G protein co
11	1914	85.6	433	23	AAU97740 Mouse TGR346a poly
12	1767	79.1	416	23	AAU97741 Mouse TGR346b poly
13	1288	56.7	245	24	AAU97741 Human G protein-co
14	508	22.7	417	21	ABP82011 Rat neuropeptide F
15	502	22.5	420	20	AAW81358 Human 7-transmembr
16	502	22.5	420	21	AAV99930 HLWAR77 polypeptid
17	502	22.5	420	21	AAV99930 Human neuropeptide
18	502	22.5	420	22	AAU00233 Orphan receptor HG
19	502	22.5	420	23	AAU79013 Human G protein-co
20	502	22.5	522	22	ABE11723 Human GPCR homolog
21	501.5	22.4	420	21	AAAB07426 Amino acid sequenc
22	501.5	22.4	522	22	AAU00234 Orphan receptor HG
23	501.5	22.4	522	24	ABP82012 Human neuropeptide
24	501.5	22.4	522	24	ABG73522 Human G-protein co
25	496	22.2	408	21	AAV76882 Human NPY-Y7 recep
26	493.5	22.1	375	24	ABG73520 D. rerio G-protein
27	479	21.4	381	16	AAV78272 Rat hippocampal ne
28	475.5	21.3	405	21	AAV76883 Mouse NPY-Y7 recep
29	474	21.2	381	16	AAV78273 Rat hippocampal ne
30	469.5	21.0	381	21	AAV58888 Human Y2 receptor
31	469.5	21.0	381	22	AAE07921 Human neuropeptide
32	469.5	21.0	381	22	AAE07957 Human neuropeptide
33	469.5	21.0	381	22	AAE06689 Human neuropeptide
34	469.5	21.0	381	22	AAE85109 Human neuropeptide
35	469.5	21.0	381	22	ABE85120 Human neuropeptide
36	469.5	21.0	381	23	ABE84500 Human hippocampus
37	469.5	21.0	381	24	ABP81858 Human neuropeptide
38	469.5	21.0	381	24	ABG73521 Human NY2R protein
39	468.5	21.0	381	19	AAW41710 Rhesus monkey neur
40	464.5	20.8	381	16	AAV78271 Human hippocampal
41	459.5	20.6	460	22	AAE61970 Rat HCRTR2 polypep
42	459.5	20.6	460	24	ABG73515 Rat OX2R protein S
43	457	20.4	444	22	AAE84416 Amino acid sequenc
44	455	20.4	444	22	AAE98007 Human hypocretin r
45	455	20.4	444	22	AAE61969 Human HCRTR2 polyp

ALIGNMENTS

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RESULT 1
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ID AAV94993 standard; Protein; 431 AA.
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AC AAV94993;
XX
DT 19-JUN-2000 (first entry)
XX
DE Human secreted protein vc38_1, SEQ ID NO:26.
XX
DE Human; secreted protein; cancer; tumour; cardiovascular disorder;
KW blood disorder; haemophilia; autoimmune disease; diabetes; inflammation;
KW infection; fungal; bacterial; viral; HIV; allergy; arthritis;
KW neurodegenerative disease; asthma; contraceptive.
OS Homo sapiens.
XX
XX WO200011015-A1.
XX
PD 02-MAR-2000.
XX
XX 24-AUG-1999; 99WO-US19351.
XX
PR 24-AUG-1998; 98US-0097638.
PR 24-AUG-1998; 98US-0097659.
PR 09-SEP-1998; 98US-0099618.
PR 28-SEP-1998; 98US-0102092.
PR 25-NOV-1998; 98US-0109978.
PR 23-DEC-1998; 98US-0113645.
PR 23-DEC-1998; 98US-0113646.
PR 23-AUG-1999; 99US-0379246.
XX

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PA (ALPH-) ALPHAGENE INC.
 XX Valenzuela D, Yuan O, Hoffman H, Hall J, Rapiejko P;
 PI WPI; 2000-224657/19.
 DR
 XX New secreted or transmembrane proteins and polynucleotides encoding
 PT them, useful for treating neurodegenerative disorders, autoimmune
 PT diseases and cancer -
 XX
 XX Claim 35; Page 284-285; 357pp; English.
 PS
 XX The invention relates to 40 human secreted proteins (AA94981-995020),
 CC and cDNA sequences encoding them (AA23423-A23462). The secreted
 CC proteins of the invention include those that are thought to be only
 CC partially secreted, i.e., transmembrane proteins. The proteins of the
 CC invention may exhibit one or more activities selected from the following:
 CC cytokine activity; cell proliferation; differentiation; immune
 CC modulation; haematopoiesis regulation; tissue growth activity;
 CC activin/inhibin activity; chemotactic/chemokinetic activity; haemostatic
 CC and thrombolytic activity; anti-inflammatory activity; and tumour
 CC inhibition activity. The proteins may be administered to patients as
 CC vaccines, and the nucleotides may be used as part of a gene therapy
 CC regime. Diseases or conditions that may be treated using the proteins or
 CC nucleotides of the invention include autoimmune diseases; genetic
 CC disorders; haemophilia; cardiovascular diseases; cancer; bacterial,
 CC fungal and viral infections, especially HIV; multiple sclerosis;
 CC rheumatoid arthritis; pulmonary inflammation; Guillain-Barre syndrome;
 CC insulin dependent diabetes mellitus; and allergic reactions such as
 CC asthma and anaemia. They may also be used for treating wounds, burns,
 CC ulcers, osteoporosis, osteoarthritis, periodontal diseases, Alzheimer's
 CC disease, Parkinson's disease, Huntington's disease and amyotrophic
 CC lateral sclerosis (ALS). Proteins with activin/inhibin activity may
 CC additionally be useful as contraceptives. Nucleic acid sequences of the
 CC invention may be used in chromosome mapping, and as a source of
 CC diagnostic primers and probes. The present sequence represents one of the
 CC 40 proteins of the invention.
 XX
 SQ Sequence 431 AA;
 Query Match 100.0%; Score 2235; DB 21; Length 431;
 Best Local Similarity 100.0%; Pred. No. 2.3e-237;
 Matches 431; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MQALNITPEQFSLRRDHNLTREQFIALYRLPLVYTPPELPGSAKLALVLTGLIFALAL 60
 DB 1 MQALNITPEQFSLRRDHNLTREQFIALYRLPLVYTPPELPGSAKLALVLTGLIFALAL 60
 QY 61 FGNALFVYVYVTRSKAMRTVTNIFICSLSLSDLLITFFCIPVTMLQNSDNLGGAFICKM 120
 DB 61 FGNALFVYVYVTRSKAMRTVTNIFICSLSLSDLLITFFCIPVTMLQNSDNLGGAFICKM 120
 QY 121 VPVQSTAVVTEILTMTCTIAVERHQGLVHPFKMKQYTNRRAPFTMLGVVWLVAVVIGSPM 180
 DB 121 VPVQSTAVVTEILTMTCTIAVERHQGLVHPFKMKQYTNRRAPFTMLGVVWLVAVVIGSPM 180
 QY 181 WHVQOLEIKYDFLYEKEHICCLEEWTSVPVHQKIYTTFFILVILFLLPLMWMLILYSKIGYE 240
 DB 181 WHVQOLEIKYDFLYEKEHICCLEEWTSVPVHQKIYTTFFILVILFLLPLMWMLILYSKIGYE 240
 QY 241 LWTIKRVGDSVLRTHGKEMSKIARKKGAIVTMVTVVALFVAVCWAPVHVHMMIEYSN 300
 DB 241 LWTIKRVGDSVLRTHGKEMSKIARKKGAIVTMVTVVALFVAVCWAPVHVHMMIEYSN 300
 QY 301 FEKEYDDVTIKMFAIVQIIGFNSNICNPVYAFMNFKNVLSAVCYVKNKTFSPAQ 360
 DB 301 FEKEYDDVTIKMFAIVQIIGFNSNICNPVYAFMNFKNVLSAVCYVKNKTFSPAQ 360
 QY 361 RHNGSGITMRRKAKFSLRENPEETKGEAFSDGNIEVKICEOTEKKLKRHLALFRSE 420
 DB 361 RHNGSGITMRRKAKFSLRENPEETKGEAFSDGNIEVKICEOTEKKLKRHLALFRSE 420
 QY 421 LAENSPDLSGH 431

DB 421 LAENSPDLSGH 431
 RESULT 2
 AAG64289
 ID AAG64289 standard; Protein; 431 AA.
 XX
 AC AAG64289;
 XX
 DT 21-SEP-2001 (first entry)
 XX
 DE Human GTP-binding protein-coupled receptor GPRV11.
 XX
 KW GTP-binding protein-coupled receptor; neuroprotective; immunomodulatory;
 KW muscular; urinary; circulatory; anorectic; human; guanosine triphosphate;
 KW G-protein.
 XX
 OS Homo sapiens.
 XX
 FN WO200148189-A1.
 PD 05-JUL-2001.
 XX
 XX 28-DEC-2000; 2000WO-JP09409.
 XX
 XX 28-DEC-1999; 99JP-0375152.
 PR 31-MAR-2000; 2000JP-0101339.
 PR 23-MAY-2000; 2000JP-0155978.
 XX
 PA (HELI-) HELIX RES INST.
 XX
 PI Matsumoto S, Oda T, Saito Y, Morikawa N, Yoshida K, Suwa M;
 PI Sugiyama T;
 XX
 DR WPI; 2001-425663/45.
 DR N-PSDB; AAA49502.
 XX
 PT Family of guanosine triphosphate binding protein coupled receptors and
 PT genes encoding them for treatment and prevention of diseases associated
 PT with these receptors -
 XX
 PS Claim 1; Pages 59-62; 137pp; Japanese.
 XX
 CC The present sequence is the protein sequence for a human guanosine
 CC triphosphate (GTP)-binding protein-coupled receptor. The receptor is
 CC useful for the investigation, diagnosis, treatment and prevention of
 CC diseases associated with GTP-binding protein-coupled receptors, including
 CC neurological, circulatory, digestive system, immune system, muscle and
 CC urinary system disorders. GTP-binding proteins are also known as
 CC G-proteins.
 XX
 SQ Sequence 431 AA;
 Query Match 100.0%; Score 2235; DB 22; Length 431;
 Best Local Similarity 100.0%; Pred. No. 2.3e-237;
 Matches 431; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MQALNITPEQFSLRRDHNLTREQFIALYRLPLVYTPPELPGSAKLALVLTGLIFALAL 60
 DB 1 MQALNITPEQFSLRRDHNLTREQFIALYRLPLVYTPPELPGSAKLALVLTGLIFALAL 60
 QY 61 FGNALFVYVYVTRSKAMRTVTNIFICSLSLSDLLITFFCIPVTMLQNSDNLGGAFICKM 120
 DB 61 FGNALFVYVYVTRSKAMRTVTNIFICSLSLSDLLITFFCIPVTMLQNSDNLGGAFICKM 120
 QY 121 VPVQSTAVVTEILTMTCTIAVERHQGLVHPFKMKQYTNRRAPFTMLGVVWLVAVVIGSPM 180
 DB 121 VPVQSTAVVTEILTMTCTIAVERHQGLVHPFKMKQYTNRRAPFTMLGVVWLVAVVIGSPM 180
 QY 181 WHVQOLEIKYDFLYEKEHICCLEEWTSVPVHQKIYTTFFILVILFLLPLMWMLILYSKIGYE 240
 DB 181 WHVQOLEIKYDFLYEKEHICCLEEWTSVPVHQKIYTTFFILVILFLLPLMWMLILYSKIGYE 240

QY	241	LWIKKRVGDSVLRTHGKEMSKIARKKKRAVIMVTVALFAVCWAPFHVHMMIEYSN	300
Db	241	LWIKKRVGDSVLRTHGKEMSKIARKKKRAVIMVTVALFAVCWAPFHVHMMIEYSN	300
QY	301	FEKEYDDVTIKMFAIVQIIGFNSICNPVIYAFMNFKNVLSAVCYCIVNKTSPAQ	360
Db	301	FEKEYDDVTIKMFAIVQIIGFNSICNPVIYAFMNFKNVLSAVCYCIVNKTSPAQ	360
QY	361	RHNSGITMWRKKAFLRENPEETKGEAFSDGNIEVKLCEOTEKKLKRHLALFRSE	420
Db	361	RHNSGITMWRKKAFLRENPEETKGEAFSDGNIEVKLCEOTEKKLKRHLALFRSE	420
QY	421	LAENSPDLSGH 431	
Db	421	LAENSPDLSGH 431	
RESULT 3			
AA	74773		
ID	AAB74773		
XX	AAB74773 standard; Protein; 431 AA.		
AC	AAB74773;		
XX			
DT	05-JUN-2001 (first entry)		
DE	Human G protein-coupled receptor protein AQ27 SEQ ID NO:1.		
XX			
KW	Human; G protein-coupled receptor; AQ27; nootropic; neuroprotective;		
KW	hypotensive; antirheumatic; antiallergic; cardiant; antianginal;		
KW	abortifacient; gene therapy; Alzheimer's disease; hypertension;		
KW	pregnancy termination; rheumatism; allergy; angina pectoris.		
XX			
OS	Homo sapiens.		
XX			
PN	WO200116316-A1.		
XX			
PD	08-MAR-2001.		
XX			
PF	24-AUG-2000; 2000WO-JP05684.		
XX			
PR	27-AUG-1999; 99JP-0241530.		
XX			
PA	(TAKE) TAKEDA CHEM IND LTD.		
XX			
PI	Watanabe T, Kikuchi K, Shintani Y;		
XX			
XX			
DR	WPI: 2001-226689/23.		
DR	N-PSDB; AAF81818, AAF81819.		
XX			
PT	Human brain-originated guanosine triphosphate protein-coupled receptor,		
PT	its salt and encoded gene, useful in (gene) diagnosis and development		
PT	of preventives and remedies for e.g. Alzheimer disease, hypertension		
PT	and rheumatism		
XX			
PS	Claim 1; Page 76-78; 84pp; Japanese.		
XX			
CC	The present sequence represents a human G protein-coupled receptor		
CC	designated AQ27. AQ27 has nootropic, neuroprotective, hypotensive,		
CC	antirheumatic, antiallergic, cardiant, antianginal and abortifacient		
CC	activities. AQ27 can be used as a G protein-coupled receptor protein		
CC	agonist. G-protein-coupled receptor signal transducer and in gene		
CC	therapy. AQ27 can be sued in the diagnosis and development of		
CC	preventives and remedies for diseases associated with dysfunction of		
CC	AQ27 e.g. Alzheimer's disease, hypertension, pregnancy termination,		
CC	rheumatism, allergy and angina pectoris.		
XX			
SQ	Sequence 431 AA;		

Query Match 100.0%; Score 2235; DB 22; Length 431;
Best Local Similarity 100.0%; Pred. No. 2.3e-237;
Matches 431; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MOALNITPEQFSRLRDLNLTREQFIALYRLRPLVVTPELPGRKALALVLTGLVIFALAL	60
Db	1	MOALNITPEQFSRLRDLNLTREQFIALYRLRPLVVTPELPGRKALALVLTGLVIFALAL	60
QY	61	FGNALVYVVTSSKAMRTVTNIFICSLALSDLLITPFCIPVTMLQNISDNWLGGAFCIKM	120
Db	61	FGNALVYVVTSSKAMRTVTNIFICSLALSDLLITPFCIPVTMLQNISDNWLGGAFCIKM	120
QY	121	VFPVOSTAVVTILMTWCIAVERHQSGLVHPFKMKQYTNRRAPTMLGVVWLVAVIVGSPM	180
Db	121	VFPVOSTAVVTILMTWCIAVERHQSGLVHPFKMKQYTNRRAPTMLGVVWLVAVIVGSPM	180
QY	181	WHVQQLLEIKYDFLYEKEHICCLEEWTSPVHQIYITTFILVILFLPLMWMLILYSKIGYE	240
Db	181	WHVQQLLEIKYDFLYEKEHICCLEEWTSPVHQIYITTFILVILFLPLMWMLILYSKIGYE	240
QY	241	LWIKKRVGDSVLRTHGKEMSKIARKKKRAVIMVTVALFAVCWAPFHVHMMIEYSN	300
Db	241	LWIKKRVGDSVLRTHGKEMSKIARKKKRAVIMVTVALFAVCWAPFHVHMMIEYSN	300
QY	301	FEKEYDDVTIKMFAIVQIIGFNSICNPVIYAFMNFKNVLSAVCYCIVNKTSPAQ	360
Db	301	FEKEYDDVTIKMFAIVQIIGFNSICNPVIYAFMNFKNVLSAVCYCIVNKTSPAQ	360
QY	361	RHNSGITMWRKKAFLRENPEETKGEAFSDGNIEVKLCEOTEKKLKRHLALFRSE	420
Db	361	RHNSGITMWRKKAFLRENPEETKGEAFSDGNIEVKLCEOTEKKLKRHLALFRSE	420
QY	421	LAENSPDLSGH 431	
Db	421	LAENSPDLSGH 431	
RESULT 4			
AA	48963		
ID	AAB48963 standard; Protein; 431 AA.		
XX			
AC	AAB48963;		
XX			
DT	27-MAR-2001 (first entry)		
XX			
DE	Human G protein-coupled receptor AXOR16.		
XX			
KW	AXOR16; human; G protein-coupled receptor; 7TM receptor;		
KW	chromosome 11q12.2; infection; viral; bacterial; fungal;		
KW	protozoan; HIV-1; HIV-2; pain; cancer; diabetes; obesity;		
KW	anorexia; bulimia; osteoporosis; asthma; allergy; urinary retention;		
KW	acute heart failure; hypotension; hypertension; angina pectoris;		
KW	myocardial infarction; stroke; ulcer; migraine; vomiting;		
KW	psychotic disorder; neurological disorder; anxiety; schizophrenia;		
KW	manic depression; bipolar disorder; depression; delirium; dementia;		
KW	severe mental retardation; dyskinesia; Parkinson's disease;		
KW	Huntington's disease; Gilles de la Tourette's syndrome; gene therapy;		
KW	vaccine; drug screening; signal transduction; ds.		
XX			
OS	Homo sapiens.		
XX			
PN	WO2000078809-A1.		
XX			
PD	28-DEC-2000.		
XX			
PF	19-JUN-2000; 2000WO-US16869.		
XX			
PR	21-JUN-1999; 99US-0337105.		
XX			
PA	(SMIK) SMITHKLINE BEECHAM CORP.		
XX			
PI	Elshourbagy N, Shabon U;		
XX			
DR	WPI: 2001-102699/11.		
DR	N-PSDB; AAC87690.		
XX			
PT	New AXOR16, a G-protein coupled receptor polypeptide for screening		

agonists and antagonists and for diagnosing and treating microbial infections, cancer, neurological disorders and asthma -

Claim 1; Page 29-30; 31pp; English.

The invention relates to the human G protein-coupled receptor AXOR16 (AAB48963) to DNA encoding AXOR16 (AAC87690), and to AXOR16 fragments and variants. Like all G protein-coupled receptors, AXOR16 has 7 putative transmembrane domains and is involved in signal transduction. AXOR16 has homology with gadus morhua neuropeptide (NPYRB) F and homology/ structural similarity with Danio rerio neuropeptide Y (NPYRYA). The human AXOR16 gene is located on chromosome 11q12.2. The invention also relates to expression vectors and host cells comprising AXOR16 DNA, to recombinant expression of AXOR16, and to an AXOR16-specific antibody. AXOR16 proteins and nucleotides may be used to treat a wide variety of disorders including bacterial, fungal, protozoal and viral infections, particularly HIV-1 or HIV-2 infections, pain; cancers; benign prostatic hypertrophy; diabetes; obesity; anorexia; bulimia; osteoporosis; asthma; allergies; urinary retention; acute heart failure; hypotension; hypertension; angina pectoris; myocardial infarction; stroke; ulcers; migraine; vomiting; psychotic and neurological disorders such as anxiety, schizophrenia, manic depression, depression, delirium, dementia, and severe mental retardation, and dyskinesias, such as Parkinson's disease, Huntington's disease or Gilles de la Tourette's syndrome. AXOR16 proteins, and nucleotides are useful as vaccines and AXOR16 proteins, nucleotides and antibodies may be used in screening compounds for their ability to modulate AXOR16 activity or expression. AXOR16 proteins are also useful for inducing an immunological response in a mammal against the above diseases, for antibody production, and to identify membrane bound or soluble receptors for AXOR16. AXOR16 nucleotides are also useful as diagnostic reagents and in chromosome localisation and tissue expression studies. The present sequence represents human AXOR16.

Sequence 431 AA;

Query Match 100.0%; Score 2235; DB 22; Length 431;
 Best Local Similarity 100.0%; Pred. No. 2.3e-237;
 Matches 431; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOALNITPEQSRLLRDHNLTRQEQIALYRLRPVLYTPELFGRAKLALVTGLIFALAL 60
 DB 1 MOALNITPEQSRLLRDHNLTRQEQIALYRLRPVLYTPELFGRAKLALVTGLIFALAL 60

QY 61 FGNALVFVYVTRSKAMRTVTWIFICSLALSLLITFFCIPVTMLQNSDNWLGAFICKM 120
 DB 61 FGNALVFVYVTRSKAMRTVTWIFICSLALSLLITFFCIPVTMLQNSDNWLGAFICKM 120

QY 121 VPFVQSTAVVTEILMTCTIAVERHOGVLPFKMKQYTNRRAPFTMLGVMLVAVVGSFM 180
 DB 121 VPFVQSTAVVTEILMTCTIAVERHOGVLPFKMKQYTNRRAPFTMLGVMLVAVVGSFM 180

QY 181 MHVQOLEIKYDFLYEKEHICCLEWTSFVHQIKYITFTLVILFLLPLMWMLLYSKTGYE 240
 DB 181 MHVQOLEIKYDFLYEKEHICCLEWTSFVHQIKYITFTLVILFLLPLMWMLLYSKTGYE 240

QY 241 LMKKRVGDSVLRTHGKEMSKARKKRAVIMMVTVALFVCAWAPPHVHMMIYSN 300
 DB 241 LMKKRVGDSVLRTHGKEMSKARKKRAVIMMVTVALFVCAWAPPHVHMMIYSN 300

QY 301 FEKEYDDVTIKMFAIVQIIGFSNSICNPVYAFNMENFKKNVLSAVCYCVNKTFSPAQ 360
 DB 301 FEKEYDDVTIKMFAIVQIIGFSNSICNPVYAFNMENFKKNVLSAVCYCVNKTFSPAQ 360

QY 361 RHGNSGITMMRKAKFSLRENPEVETKGBAPSDGNIKVLCBQTEKKLKRHLALPRSE 420
 DB 361 RHGNSGITMMRKAKFSLRENPEVETKGBAPSDGNIKVLCBQTEKKLKRHLALPRSE 420

QY 421 LAENSPDLSGH 431
 DB 421 LAENSPDLSGH 431

RESULT 5

AAU97735

ID AAU97735 standard; Protein; 431 AA.

XX AC AAU97735;

XX 27-AUG-2002 (first entry)

XX Human TGR346 polypeptide.

XX Human; TGR346; receptor; G-protein coupled receptor; GPCR; TGR;

XX TGR-associated disorder; signal transduction; renal failure; nephritis;

XX hypothyroidism; hypogonadism; retinitis pigmentosa; growth disorder;

XX diabetes insipidus; hyperprolactinaemia; thirst disturbance; appetite;

XX sleep disturbance; temperature regulation; blood pressure; hypothalamus;

XX circadian rhythm.

XX Homo sapiens.

XX WO200242458-A2.

XX 30-MAY-2002.

XX 21-NOV-2001; 2001WO-US43404.

XX 22-NOV-2000; 2000US-252841P.

XX 22-DEC-2000; 2000US-257636P.

XX 12-JAN-2001; 2001US-261377P.

XX 28-MAR-2001; 2001US-279554P.

XX 29-MAR-2001; 2001US-280696P.

XX (TULA-) TULARIK INC.

XX Tian H, Zhao J, Chen J, Cutler G, An S, Dai K, Gupte JS;

XX WPI; 2002-463633/49.

XX N-PSDB; ABK86287.

XX New isolated G-protein coupled receptor polypeptide, termed TGR, for

XX diagnosis and treatment of diseases such as renal failure, nephritis,

XX hypothyroidism, diabetes insipidus, and disturbances of thirst and

XX sleep -

XX Claim 33; Page 74; 98pp; English.

XX The invention relates to a G-protein coupled receptor polypeptide (GPCR),

XX termed TGR, and its associated nucleic acid. The sequences of the

XX invention are useful for identifying a compound that modulates signal

XX transduction and for identifying a mammal having a TGR-associated

XX disorder. The proteins and nucleic acids are useful in diagnosis and

XX treatment of diseases or conditions such as renal failure, nephritis,

XX hypothyroidism, hypogonadism, retinitis pigmentosa, growth disorders,

XX diabetes insipidus, hyperprolactinaemia and disturbances of thirst,

XX sleep, temperature regulation, appetite, blood pressure or any other

XX syndrome or disease associated with the hypothalamus. The sequences can

XX be used in regulation of circadian rhythms, for use as genetic markers

XX for the identification of mutations associated with diseases resulting

XX from GPCR inactivation in particular cell types and for identification of

XX modulators of GPCR signal transduction. This sequence represents the

XX human TGR346 polypeptide.

XX Sequence 431 AA;

Query Match 100.0%; Score 2235; DB 23; Length 431;
 Best Local Similarity 100.0%; Pred. No. 2.3e-237;
 Matches 431; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOALNITPEQSRLLRDHNLTRQEQIALYRLRPVLYTPELFGRAKLALVTGLIFALAL 60
 DB 1 MOALNITPEQSRLLRDHNLTRQEQIALYRLRPVLYTPELFGRAKLALVTGLIFALAL 60

QY 61 FGNALVFVYVTRSKAMRTVTWIFICSLALSLLITFFCIPVTMLQNSDNWLGAFICKM 120

Db 61 FGNALVYVTVTRSKAMRTVTNIFCSIALSDLLITPFCIPVTMLQNLSDNWLGAFICKM 120
 QY 121 VPFVQSTAVVTEILTMTCTIAVERHQGLVHPFKMKQYTNRRRAFTMLGVVWLVAIVVGSMP 180
 Db 121 VPFVQSTAVVTEILTMTCTIAVERHQGLVHPFKMKQYTNRRRAFTMLGVVWLVAIVVGSMP 180
 QY 181 WHVQOLEIKYDFLYEKEHICCLSEWTSVPHQKIYTTFFILVILFLLPLVWMLLYSKIGYE 240
 Db 181 WHVQOLEIKYDFLYEKEHICCLSEWTSVPHQKIYTTFFILVILFLLPLVWMLLYSKIGYE 240
 QY 241 LWIKKRVGDSGLRTTHGKEMSKIARKKRAVIMMVTVVALFAVCWAPFVHVHMIEYGN 300
 Db 241 LWIKKRVGDSGLRTTHGKEMSKIARKKRAVIMMVTVVALFAVCWAPFVHVHMIEYGN 300
 QY 301 FEKEYDDVTIKMIFAIQIIGFNSINCPNIVYAFMNFENPKKNVLSAVCYIVNKTSPAQ 360
 Db 301 FEKEYDDVTIKMIFAIQIIGFNSINCPNIVYAFMNFENPKKNVLSAVCYIVNKTSPAQ 360
 QY 361 RHGNSGITMWRKKAFFSLRENPEETKGEAFSDGNIETVKLCEQTEKKLKRHLALFRSE 420
 Db 361 RHGNSGITMWRKKAFFSLRENPEETKGEAFSDGNIETVKLCEQTEKKLKRHLALFRSE 420
 QY 421 LAENSPDLSGH 431
 Db 421 LAENSPDLSGH 431

RESULT 6

AAU76035
 ID AAU76035 standard; Protein; 431 AA.

XX AC AAU76035;
 XX DT 08-MAY-2002 (first entry)

XX DE Human neuropeptide Y-like GPCR (NPY-like GPCR) protein sequence.

XX KW Human; neuropeptide Y-like G protein-coupled; receptor; antibody;
 KW NPY-like GPCR; anorectic; antidiabetic; tranquilizer; hypertensive;
 KW hypotensive; analgesic; cytotatic; antiaesthetic; osteopathic;
 KW cardiovascular; antitumor; neotropic; anticonvulsant; antiallergic;
 KW neuroleptic; antidote; antiparkinsonian; neuroprotective; gene therapy;
 KW antidepressant; antiaesthetic; diuretic; chromosome 11q12.2.

XX OS Homo sapiens.

XX PN WO200204518-A2.

XX PD 17-JAN-2002.

XX PF 06-JUL-2001; 2001WO-US21276.

XX PR 06-JUL-2000; 2000US-216523P.

XX PA (FARB) BAYER CORP.

XX PI Bloomquist BT, Zhelein L;

XX DR WPI; 2002-148166/19.

XX DR N-PSDB; ABK14956.

XX PT New neuropeptide Y-like G protein-coupled receptor, for detecting

PT regulators for preventing, ameliorating, or correcting e.g. obesity,

PT anorexia, diabetes, hypotension, hypertension, pain, cancers, or

PT neurological disorders

PS Claim 10; Fig 1; 91pp; English.

XX CC The present invention relates to a new polynucleotide encoding a

CC polypeptide neuropeptide Y-like G protein-coupled receptor (NPY-like

CC GPCR), comprising a 431 amino acid sequence, given in the specification.

CC The polynucleotide of the invention is used to produce a NPY-like GPCR

CC polypeptide. The complement of the polynucleotide can be used to detect

CC a coding sequence for a NPY-like GPCR. A reagent, preferably an antibody,
 CC that binds to NPY-like GPCR can be used to detect it. The NPY-like GPCR
 CC can be used to screen for agents that can regulate the activity of it. A
 CC reagent that binds to or regulates NPY-like GPCR can be used to reduce
 CC the biological activity of NPY-like GPCR, or treat a disorder associated
 CC with abnormal expression of NPY-like GPCR. The reagent is useful for
 CC preventing, ameliorating or correcting dysfunction or diseases such as
 CC obesity, anorexia, bulimia, diabetes, hypotension, hypertension, cocaine
 CC withdrawal, pain, cancers, asthma, urinary retention, osteoporosis,
 CC angina pectoris, myocardial infarction, ulcers, allergies, congestive
 CC heart failure, memory enhancement, cardiac and cerebral vasospasm,
 CC pheochromocytoma, ganglioneuroblastoma, Huntington's disease, severe
 CC mental retardation, Alzheimer's disease, Parkinson's disease, psychotic
 CC and neurological disorders including anxiety, schizophrenia, manic
 CC depression, delirium, dementia and dyskinesias. The polypeptide may also
 CC be used in raising specific antibodies. The present amino acid sequence
 CC represents human NPY-like GPCR protein of the invention. This protein is
 CC encoded by the human NPY-like GPCR gene located on chromosome 11q12.2.

XX SQ Sequence 431 AA;

Query Match 100.0%; Score 2235; DB 23; Length 431;
 Best Local Similarity 100.0%; Pred. NO. 2.3e-237;
 Matches 431; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQALNITPEQFSRLLRDHNLTREQFIALYRLRPLVYTPPELPGRAKLALVLTGVLFALAL 60
 Db 1 MQALNITPEQFSRLLRDHNLTREQFIALYRLRPLVYTPPELPGRAKLALVLTGVLFALAL 60

QY 61 FGNALVYVTVTRSKAMRTVTNIFCSIALSDLLITPFCIPVTMLQNLSDNWLGAFICKM 120
 Db 61 FGNALVYVTVTRSKAMRTVTNIFCSIALSDLLITPFCIPVTMLQNLSDNWLGAFICKM 120

QY 121 VPFVQSTAVVTEILTMTCTIAVERHQGLVHPFKMKQYTNRRRAFTMLGVVWLVAIVVGSMP 180
 Db 121 VPFVQSTAVVTEILTMTCTIAVERHQGLVHPFKMKQYTNRRRAFTMLGVVWLVAIVVGSMP 180

QY 181 WHVQOLEIKYDFLYEKEHICCLSEWTSVPHQKIYTTFFILVILFLLPLVWMLLYSKIGYE 240
 Db 181 WHVQOLEIKYDFLYEKEHICCLSEWTSVPHQKIYTTFFILVILFLLPLVWMLLYSKIGYE 240

QY 241 LWIKKRVGDSGLRTTHGKEMSKIARKKRAVIMMVTVVALFAVCWAPFVHVHMIEYGN 300
 Db 241 LWIKKRVGDSGLRTTHGKEMSKIARKKRAVIMMVTVVALFAVCWAPFVHVHMIEYGN 300

QY 301 FEKEYDDVTIKMIFAIQIIGFNSINCPNIVYAFMNFENPKKNVLSAVCYIVNKTSPAQ 360
 Db 301 FEKEYDDVTIKMIFAIQIIGFNSINCPNIVYAFMNFENPKKNVLSAVCYIVNKTSPAQ 360

QY 361 RHGNSGITMWRKKAFFSLRENPEETKGEAFSDGNIETVKLCEQTEKKLKRHLALFRSE 420
 Db 361 RHGNSGITMWRKKAFFSLRENPEETKGEAFSDGNIETVKLCEQTEKKLKRHLALFRSE 420

QY 421 LAENSPDLSGH 431
 Db 421 LAENSPDLSGH 431

RESULT 7
 ABG73503
 ID ABG73503 standard; Protein; 431 AA.

XX AC ABG73503;
 XX DT 14-FEB-2003 (first entry)

XX DE Human G protein coupled receptor HGPBMY2 SEQ ID 17.

XX KW Human; G-protein coupled receptor; HGPBMY1; HGPBMY2; immunosuppressive;
 KW cardiac; neuroprotective; antiinflammatory; cytostatic; vulnery;

KW vaccine; gene therapy; autoimmune; cardiovascular; neural; reproductive;

KW haematopoietic; pulmonary; gastrointestinal; proliferation; cell cycle;

KW birth defect; aberrant phosphorylation; acute phase response; receptor;

KW signal transduction; hyperimmune activity; inflammatory; hypercongenital;
 KW necrotic lesion; wound; organ transplant rejection.
 XX Homo sapiens.
 OS
 XX WO200268591-A2.
 PN
 XX 06-SEP-2002.
 PD
 XX 22-FEB-2002; 2002WO-US05281.
 PF
 XX 23-FEB-2001; 2001US-270792P.
 PR
 XX 23-FEB-2001; 2001US-270793P.
 PR
 XX 06-JUN-2001; 2001US-296427P.
 PR
 XX (BRIM) BRISTOL-MYERS SQUIBB CO.
 PA
 XX Feder J, Ramanathan C, Nelson T, Mintier G, Cacace A, Barber L;
 PI Kornacker M, Bol D;
 XX
 XX WPI; 2003-058304/05.
 DR
 XX N-PSDB; ABS57631.
 DR
 XX New human HGPBMY1 or HGPBMY2 polynucleotide and polypeptide, useful
 XX preventing, treating or ameliorating a disorder e.g., wound,
 PT cardiovascular disorder or transplant rejection -
 PT
 XX
 XX Claim 5; Figure 7; 316pp; English.
 PS
 XX This invention describes the novel human G-protein coupled receptors
 CC (GPCR's), HGPBMY1 or HGPBMY2 which have immunosuppressive, cardiant,
 CC neuroprotective, antiinflammatory, cytostratic and vulnerary activity
 CC and can be used in vaccines or for gene therapy. Pharmaceutical
 CC compositions comprising HGPBMY1 or HGPBMY2 polypeptides or their
 CC agonists or antagonists or modulators, or a HGPBMY1- or
 CC HGPBMY2-specific antibody are useful for preventing, treating or
 CC ameliorating a medical condition comprising autoimmune, cardiovascular,
 CC neural, reproductive, haematopoietic, pulmonary, gastrointestinal or
 CC proliferating disorder, a cell cycle or birth defect, a disorder related
 CC to aberrant phosphorylation, acute phase responses or signal transduction
 CC or to hyperimmune activity, an inflammatory or hypercongenital condition,
 CC a necrotic lesion, a wound, organ transplant rejection or a condition
 CC related to organ transplant rejection. This sequence represents the human
 CC HGPBMY2 protein described in the disclosure of the invention.
 XX
 XX Sequence 431 AA;
 SQ
 Query Match 100.0%; Score 2235; DB 24; Length 431;
 Best Local Similarity 100.0%; Pred. No. 2.3e-237;
 Matches 431; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MQALNITPEQSRLLRDHNLTRQFIYALYRLPLVYTPPELGRKALVLTGVLIFAL 60
 DB 1 MQALNITPEQSRLLRDHNLTRQFIYALYRLPLVYTPPELGRKALVLTGVLIFAL 60
 QY 61 FGNALVYVYTRSKAMRTVNIIFCSIALSDLLITFPFCIPVTMLQNSDNLGGAFCIKM 120
 DB 61 FGNALVYVYTRSKAMRTVNIIFCSIALSDLLITFPFCIPVTMLQNSDNLGGAFCIKM 120
 QY 121 VPVQSTAVVTEILTMTCAVERHQGLVHPFKMKQYTNRRAPFTMLGVVWLVAIVGSPM 180
 DB 121 VPVQSTAVVTEILTMTCAVERHQGLVHPFKMKQYTNRRAPFTMLGVVWLVAIVGSPM 180
 QY 181 WHVQOLEKIDVLEKEHICCLEBWSPVHOKIYTTFFILVILFLPLMWMLILSKIGYE 240
 DB 181 WHVQOLEKIDVLEKEHICCLEBWSPVHOKIYTTFFILVILFLPLMWMLILSKIGYE 240
 QY 241 LWIKRVGDSGLVLTTHGKMSKIFARKKGAIVIMVTVVALFAVCWAPPHVVMIEYSN 300
 DB 241 LWIKRVGDSGLVLTTHGKMSKIFARKKGAIVIMVTVVALFAVCWAPPHVVMIEYSN 300
 QY 301 FEKEYDDVTIKMIFAIQIIGFNSICNPITVYAFMNFKNVLSAVCYCIUNKTFSPAQ 360
 DB 301 FEKEYDDVTIKMIFAIQIIGFNSICNPITVYAFMNFKNVLSAVCYCIUNKTFSPAQ 360

Db 301 FEKEYDDVTIKMIFAIQIIGFNSICNPITVYAFMNFKNVLSAVCYCIUNKTFSPAQ 360
 QY 361 RHGNSGITMRRKAKFSLRENPFVETKGEAFSDGNIIEVKLCEQTEKKKLRHIALPRSE 420
 Db 361 RHGNSGITMRRKAKFSLRENPFVETKGEAFSDGNIIEVKLCEQTEKKKLRHIALPRSE 420
 QY 421 LAENSPDLSGH 431
 Db 421 LAENSPDLSGH 431
 RESULT 8
 AAY71309
 ID AAY71309 standard; Protein; 431 AA.
 XX
 AC AAY71309;
 XX
 DT 02-NOV-2000 (first entry)
 XX Human orphan G protein-coupled receptor hrUP4.
 DE
 XX Human; orphan G protein-coupled receptor; GPCR; hrUP4; drug screening;
 KW transmembrane receptor; expressed sequence tag; EST; signal cascade.
 KW
 XX Homo sapiens.
 OS
 XX WO200031258-A2.
 FN
 XX 02-JUN-2000.
 PD
 XX 13-OCT-1999; 99WO-US23687.
 PF
 XX 20-NOV-1998; 98US-0109213.
 PR 16-FEB-1999; 99US-0120416.
 PR 26-FEB-1999; 99US-0121852.
 PR 12-MAR-1999; 99US-0123946.
 PR 12-MAR-1999; 99US-0123949.
 PR 28-MAY-1999; 99US-0136436.
 PR 28-MAY-1999; 99US-0136437.
 PR 28-MAY-1999; 99US-0136439.
 PR 28-MAY-1999; 99US-0137127.
 PR 28-MAY-1999; 99US-0137131.
 PR 29-JUN-1999; 99US-0141448.
 PR 29-SEP-1999; 99US-0156555.
 PR 29-SEP-1999; 99US-0156633.
 PR 29-SEP-1999; 99US-0156634.
 PR 29-SEP-1999; 99US-0156653.
 PR 01-OCT-1999; 99US-0157280.
 PR 01-OCT-1999; 99US-0157281.
 PR 01-OCT-1999; 99US-0157282.
 PR 01-OCT-1999; 99US-0157293.
 PR 01-OCT-1999; 99US-0157294.
 PR 12-OCT-1999; 99US-0416760.
 PR 12-OCT-1999; 99US-0417044.
 XX (AREN-) ARENA PHARM INC.
 PA
 XX Chen R, Bang HT, Liaw CW, Lin I;
 PI
 XX WPI; 2000-400068/34.
 DR N-PSDB; AAD01136.
 DR
 XX Novel human orphan G protein-coupled receptors and the encoding cDNAs
 PT for use in the identification of G protein-coupled receptor agonists -
 PT
 XX Claim 74; Page 89-91; 102pp; English.
 PS
 XX The present amino acid sequence is the hrUP4, an endogenous human
 CC orphan G protein-coupled receptor (GPCR). The full length hrUP4 cDNA was
 CC cloned by RT-PCR with human brain cDNA as template. The hrUP4 PCR
 CC fragment obtained was an alternatively spliced form of the EST (expressed
 CC sequence tag) clone AI307658. The orphan GPCR of the invention, like

CC all GPCRs has seven transmembrane alpha helices with an extracellular
 CC N-terminus and an intracellular C-terminus. However, no endogenous
 CC ligands has yet been identified for the proteins of the invention. The
 CC orphan GPCRs may be used in the identification of their endogenous
 CC ligands, and to screen potential GPCR agonists and antagonists for use as
 CC pharmaceutical agents. The proteins may also be used in the study of
 CC GPCR-mediated signalling cascades, and to elucidate their precise role in
 CC normal and diseased human conditions. Nucleic acid encoding human orphan
 CC GPCRs may be used for tissue localisation expression analysis to provide
 CC information about their function in healthy and pathological states.
 XX
 SQ Sequence 431 AA;

Query Match 99.9%; Score 2232; DB 21; Length 431;
 Best Local Similarity 99.8%; Pred. No. 4.9e-237;
 Matches 430; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQALNITPEQSRLLRDHNLTRQFIALYRLPLVYTPPELPGRAKLALVLTGVLIIFALAL 60
 DB 1 MQALNITPEQSRLLRDHNLTRQFIALYRLPLVYTPPELPGRAKLALVLTGVLIIFALAL 60
 QY 61 FGNALVFYVTVTRSKAMRTVTNIFICSLSALSDLLITFFCIPVTMLQNSDNWLGGAFCIKM 120
 DB 61 FGNALVFYVTVTRSKAMRTVTNIFICSLSALSDLLITFFCIPVTMLQNSDNWLGGAFCIKM 120
 QY 121 VPFFQSTAVVTEILTMTCIAVERHOGVLVHPFKMKQVYTNERRAFTMLGVVWLVAVIVGSPM 180
 DB 121 VPFFQSTAVVTEILTMTCIAVERHOGVLVHPFKMKQVYTNERRAFTMLGVVWLVAVIVGSPM 180
 QY 181 WHVQOLEIKYDFLYEKEHICCLEEWTSFVHQKIYTTTILVILFLLPLVMWLIYSKIGYE 240
 DB 181 WHVQOLEIKYDFLYEKEHICCLEEWTSFVHQKIYTTTILVILFLLPLVMWLIYSKIGYE 240
 QY 241 LWIKKRVGDGSLVLRTHGKEMSKIARKKRAVINMMVTWVAFVAVVAVVHMMIEYSN 300
 DB 241 LWIKKRVGDGSLVLRTHGKEMSKIARKKRAVINMMVTWVAFVAVVAVVHMMIEYSN 300

22-AUG-2000 (first entry)
 Human G protein coupled receptor hRUP4 protein SEQ ID NO:40.
 Human; G protein coupled receptor; GPCR; transmembrane receptor;
 identification; agonist; screening; therapeutic; pharmaceutical;
 mutant.
 OS Homo sapiens.
 XX WO200022131-A2.
 XX 20-APR-2000.
 XX 13-OCT-1999; 99WO-US24065.
 XX 13-OCT-1998; 98US-0170496.

PR 12-NOV-1998; 98US-0108029.
 PR 20-NOV-1998; 98US-0109213.
 PR 27-NOV-1998; 98US-0110060.
 PR 16-FEB-1999; 99US-0120416.
 PR 26-FEB-1999; 99US-0121852.
 PR 12-MAR-1999; 99US-0123944.
 PR 12-MAR-1999; 99US-0123945.
 PR 12-MAR-1999; 99US-0123946.
 PR 12-MAR-1999; 99US-0123948.
 PR 12-MAR-1999; 99US-0123949.
 PR 12-MAR-1999; 99US-0123951.
 PR 28-MAY-1999; 99US-0136436.
 PR 28-MAY-1999; 99US-0136437.
 PR 28-MAY-1999; 99US-0136439.
 PR 28-MAY-1999; 99US-0137127.
 PR 28-MAY-1999; 99US-0137131.
 PR 30-JUN-1999; 99US-0137567.
 PR 27-AUG-1999; 99US-0141448.
 PR 03-SEP-1999; 99US-0151114.
 PR 29-SEP-1999; 99US-0152524.
 PR 29-SEP-1999; 99US-0156633.
 PR 29-SEP-1999; 99US-0156655.
 PR 29-SEP-1999; 99US-0156634.
 XX (AREN-) ARENA PHARM INC.
 PA Behan DP, Lehmann-Bruinsma K, Chalmers DT, Chen R, Dang HT;
 PI Gore M, Liaw CW, Lin I, Lowitz K, White C;
 XX WPI; 2000-317986/27.
 DR N-PSDB; AAA46037.
 XX Non-endogenous, human G protein-coupled receptors for screening
 PT receptor, inverse or partial agonists useful as therapeutic agents -
 XX Example 1; Page 119-120; 187pp; English.
 PS The present invention describes transmembrane receptors, preferably
 CC human G protein coupled receptors (GPCR), for which the endogenous
 CC ligand is unknown (orphan GPCR receptors). More specifically the present
 CC invention relates to non-endogenous, constitutively activated versions
 CC of a human GPCR. These non-endogenous human GPCRs can be useful for
 CC the direct identification of candidate compounds as receptor agonists,
 CC inverse agonists or partial agonists for use as pharmaceutical agents.
 CC AAA46017 to AAA46126 and AAB02825 to AAB02859 represent sequences used in
 CC the exemplification of the present invention.
 XX
 SQ Sequence 431 AA;

Query Match 99.9%; Score 2232; DB 21; Length 431;
 Best Local Similarity 99.8%; Pred. No. 4.9e-237;
 Matches 430; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQALNITPEQSRLLRDHNLTRQFIALYRLPLVYTPPELPGRAKLALVLTGVLIIFALAL 60
 DB 1 MQALNITPEQSRLLRDHNLTRQFIALYRLPLVYTPPELPGRAKLALVLTGVLIIFALAL 60
 QY 61 FGNALVFYVTVTRSKAMRTVTNIFICSLSALSDLLITFFCIPVTMLQNSDNWLGGAFCIKM 120
 DB 61 FGNALVFYVTVTRSKAMRTVTNIFICSLSALSDLLITFFCIPVTMLQNSDNWLGGAFCIKM 120
 QY 121 VPFFQSTAVVTEILTMTCIAVERHOGVLVHPFKMKQVYTNERRAFTMLGVVWLVAVIVGSPM 180
 DB 121 VPFFQSTAVVTEILTMTCIAVERHOGVLVHPFKMKQVYTNERRAFTMLGVVWLVAVIVGSPM 180
 QY 181 WHVQOLEIKYDFLYEKEHICCLEEWTSFVHQKIYTTTILVILFLLPLVMWLIYSKIGYE 240
 DB 181 WHVQOLEIKYDFLYEKEHICCLEEWTSFVHQKIYTTTILVILFLLPLVMWLIYSKIGYE 240
 QY 241 LWIKKRVGDGSLVLRTHGKEMSKIARKKRAVINMMVTWVAFVAVVAVVHMMIEYSN 300
 DB 241 LWIKKRVGDGSLVLRTHGKEMSKIARKKRAVINMMVTWVAFVAVVAVVHMMIEYSN 300

QY 301 FEKEYDDVTIKMFAIVQIIIGFSNSICNPIVYAFMNFKNVLSAVCYCIWNKTFSPAQ 360
 |||||
 DB 301 FEKEYDDVTIKMFAIVQIIIGFSNSICNPIVYAFMNFKNVLSAVCYCIWNKTFSPAQ 360
 |||||
 QY 361 RHNGSGITMRKKAFLRENPVETKGEAFSDGNIEVKLCEOTEKPKLKRHLALFRSE 420
 |||||
 DB 361 RHNGSGITMRKKAFLRENPVETKGEAFSDGNIEVKLCEOTEKPKLKRHLALFRSE 420
 |||||
 QY 421 LAENSPDLSGH 431
 |||||
 DB 421 LAENSPDLSGH 431
 |||||

RESULT 10

AA02853
 ID AAB02853 standard; Protein; 431 AA.

XX AC AAB02853;

DT 22-AUG-2000 (first entry)

XX DE Human G protein coupled receptor hRUP4 (V272K) protein SEQ ID NO:128.

XX KW Human; G protein coupled receptor; GPCR; transmembrane receptor;
 KW identification; agonist; screening; therapeutic; pharmaceutical;
 KW mutant.

XX OS Homo sapiens.

OS Synthetic.

XX WO2000022131-A2.

XX 20-APR-2000.

PF 13-OCT-1999; 99WO-US24065.

XX 13-OCT-1998; 98US-0170496.

PR 12-NOV-1998; 98US-0108029.

PR 20-NOV-1998; 98US-0109213.

PR 27-NOV-1998; 98US-0110060.

PR 16-FEB-1999; 98US-0120416.

PR 26-FEB-1999; 98US-0121852.

PR 12-MAR-1999; 98US-0123944.

PR 12-MAR-1999; 98US-0123946.

PR 12-MAR-1999; 98US-0123948.

PR 12-MAR-1999; 98US-0123949.

PR 28-MAY-1999; 98US-0136436.

PR 28-MAY-1999; 98US-0136437.

PR 28-MAY-1999; 98US-0136439.

PR 28-MAY-1999; 98US-0137127.

PR 28-MAY-1999; 98US-0137131.

PR 30-JUN-1999; 98US-0137567.

PR 27-AUG-1999; 98US-0151114.

PR 03-SEP-1999; 98US-0152524.

PR 28-SEP-1999; 98US-0152633.

PR 28-SEP-1999; 98US-0156555.

PR 29-SEP-1999; 98US-0156634.

XX (AREN-) ARENA PHARM INC.

XX Behan DP, Lehmann-Bruinsma K, Chalmers DT, Chen R, Dang HT;

PI Gore M, Liaw CW, Lin I, Lowitz K, White C;

PI WPI; 2000-317986/27.

DR N-PSDB; AAB46115.

XX Non-endogenous, human G protein-coupled receptors for screening

PT receptor, inverse or partial agonists useful as therapeutic agents

XX Example 2; Page 164-166; 187pp; English.

PS

XX The present invention describes transmembrane receptors, preferably
 CC human G protein coupled receptors (GPCR), for which the endogenous
 CC ligand is unknown (orphan GPCR receptors). More specifically the present
 CC invention relates to non-endogenous, constitutively activated versions
 CC of a human GPCR. These non-endogenous human GPCRs can be useful for
 CC the direct identification of candidate compounds as receptors agonists,
 CC inverse agonists or partial agonists for use as pharmaceutical agents.
 CC AAB46017 to AAB46126 and AAB02825 to AAB02899 represent sequences used in
 CC the exemplification of the present invention.

XX SQ Sequence 431 AA;

Query Match 99.6%; Score 2226; DB 21; Length 431;
 Best Local Similarity 99.5%; Pred. No. 2.3e-236;
 Matches 429; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MQALNITPEQFSRLDRDHLTREQFIALYRLRPLVYTPPELPGRAKALVLTGVLIFALAL 60
 |||||
 DB 1 MQALNITPEQFSRLDRDHLTREQFIALYRLRPLVYTPPELPGRAKALVLTGVLIFALAL 60
 |||||
 QY 61 FGNALVFYVTRSKAMRTVTNIFICSLALSDLLITFFCIPVTMLQNIISDNMLGGAFICKM 120
 |||||
 DB 61 FGNALVFYVTRSKAMRTVTNIFICSLALSDLLITFFCIPVTMLQNIISDNMLGGAFICKM 120
 |||||
 QY 121 VPFVOSTAVVTEILTWTCTIAVERHQGLVHPFKKKQYTNRAFTMLGVVWLVAVTVGSPM 180
 |||||
 DB 121 VPFVOSTAVVTEILTWTCTIAVERHQGLVHPFKKKQYTNRAFTMLGVVWLVAVTVGSPM 180
 |||||
 QY 181 WHVQOLEIKYDFLYEKEHEHICCLEEWTSPVHQKIYITFTILVILFLPLMVLILYSKIGYE 240
 |||||
 DB 181 WHVQOLEIKYDFLYEKEHEHICCLEEWTSPVHQKIYITFTILVILFLPLMVLILYSKIGYE 240
 |||||
 QY 241 LWTIKRVGDSVLTTHGKEMSKIAKKYRAVIMVTVVAVFACWAPVHVMMIEYSN 300
 |||||
 DB 241 LWTIKRVGDSVLTTHGKEMSKIAKKYRAVIMVTVVAVFACWAPVHVMMIEYSN 300
 |||||
 QY 301 FEKEYDDVTIKMFAIVQIIIGFSNSICNPIVYAFMNFKNVLSAVCYCIWNKTFSPAQ 360
 |||||
 DB 301 FEKEYDDVTIKMFAIVQIIIGFSNSICNPIVYAFMNFKNVLSAVCYCIWNKTFSPAQ 360
 |||||
 QY 361 RHNGSGITMRKKAFLRENPVETKGEAFSDGNIEVKLCEOTEKPKLKRHLALFRSE 420
 |||||
 DB 361 RHNGSGITMRKKAFLRENPVETKGEAFSDGNIEVKLCEOTEKPKLKRHLALFRSE 420
 |||||
 QY 421 LAENSPDLSGH 431
 |||||
 DB 421 LAENSPDLSGH 431
 |||||

RESULT 11

AAU97740
 ID AAU97740 standard; Protein; 433 AA.

XX AC AAU97740;

DT 27-AUG-2002 (first entry)

XX DE Mouse TGR346a polypeptide.

XX Mouse; TGR346a; receptor; G-protein coupled receptor; GPCR; TGR;

KW TGR-associated disorder; signal transduction; renal failure; nephritis;

KW hypothyroidism; hypogonadism; retinitis pigmentosa; growth disorder;

KW diabetes insipidus; hyperprolactinemia; thirst disturbance; appetite;

KW sleep disturbance; temperature regulation; blood pressure; hypothalamus;

KW circadian rhythm.

XX Mus sp.

XX WO200242458-A2.

XX 30-MAY-2002.

PF 21-NOV-2001; 2001WO-US43404.
 XX 22-NOV-2000; 2000US-252841P.
 PR 22-DEC-2000; 2000US-257636P.
 PR 12-JAN-2001; 2001US-261377P.
 PR 28-MAR-2001; 2001US-279554P.
 PR 29-MAR-2001; 2001US-280696P.
 XX (TULA-) TULARIK INC.
 XX Tian H, Zhao J, Chen J, Cutler G, An S, Dai K, Gupte JS;
 XX WPI: 2002-463633/49.
 DR N-PSDB; ABK86292.
 XX New isolated G-protein coupled receptor polypeptide, termed TGR, for
 PT diagnosis and treatment of diseases such as renal failure, nephritis,
 PT hypothyroidism, diabetes insipidus, and disturbances of thirst and
 PT sleep -
 XX
 PS Claim 29; Page 78; 98pp; English.
 CC The invention relates to a G-protein coupled receptor polypeptide (GPCR),
 CC termed TGR, and its associated nucleic acid. The sequences of the
 CC invention are useful for identifying a compound that modulates signal
 CC transduction and for identifying a mammal having a TGR-associated
 CC disorder. The proteins and nucleic acids are useful in diagnosis and
 CC treatment of diseases or conditions such as renal failure, nephritis,
 CC hypothyroidism, hypogonadism, retinitis pigmentosa, growth disorders,
 CC diabetes insipidus, hyperprolactinemia and disturbances of thirst,
 CC sleep, temperature regulation, appetite, blood pressure or any other
 CC syndrome or disease associated with the hypothalamus. The sequences can
 CC be used in regulation of circadian rhythms, for use as genetic markers
 CC for the identification of mutations associated with diseases resulting
 CC from GPCR inactivation in particular cell types and for identification of
 CC modulators of GPCR signal transduction. This sequence represents the
 CC mouse TGR346a polypeptide.
 XX Sequence 433 AA;
 SQ
 Query Match 85.6%; Score 1914; DB 23; Length 433;
 Best Local Similarity 83.5%; Pred. No. 5.9e-202;
 Matches 360; Conservative 27; Mismatches 44; Indels 0; Gaps 0;
 QY 1 MQALNITPQFGRLLARDHNLREQFTALYRLPLVYTPELPGRKALVLVGLVIFALAL 60
 DB 1 MQALNITAPQFGRLLSAHNLREQFTIHYRLPLVYTPELPGRKALVLVGLVIFALAL 60
 QY 61 FGNALVYVYVTSKAMRTVTNIFCSLALSDLLITFFCIPVTMLQNI SDNMLGGAFICKM 120
 DB 61 FGNLSVYVYVTSKAMRTVTNIFCSLALSDLLIAFFCIPVTMLQNI SDKWLGGAFICKM 120
 QY 121 VFPVQSTAVVTEILTMTCLAVRHHQGLVHPFKMKQYTNRAFTMLGVVVLVAVTVGSPM 180
 DB 121 VFPVQSTAVVTEILTMTCLAVRHHQGLIHPFKMKQYTNRAFTMLGVVVLVAVTVGSPM 180
 QY 181 WHVQLEIKYDFLYEKEHCCLBEWSPHQKIYTFILVILFLPLMWMLLYSKIGYE 240
 DB 181 WHVQLEIKYDFLYEKEHCCLBEWSPHQKIYTFILVILFLPLMWMLLYSKIGYE 240
 QY 241 LWTIKRVGDSVLRTTHGKEMSKIAKKKRVMTVMVTVVALFVAVCWAPPHVHHMIEYSN 300
 DB 241 LWTIKRVGSSALQTHGKEMSKIAKKKRVMTVMVTVVALFVAVCWAPPHVHHMIEYSN 300
 QY 301 FEKEYDDVTIKMIFAIYVQIIGFSNSICNPVYAFNMENFKKNVLGSAVCYCIYVNTFTSPAQ 360
 DB 301 FEKEYDDVTIKMIFAVAQTIIGFNSICNPVYAFNMENFKKNVLGSAVCYCIYVNTFTSPAQ 360
 QY 361 RHGNSGITMWRKAKSLRENPEETKGAFTSDGNIEVKLCQTEKKKXKHLALPSE 420
 DB 361 KPGNSGISMMOKKAKLSRQRPVAAEKGLFSDANVDVKLCQCEKQKQLQALPSE 420
 QY 421 LAENSPDLSGH 431

DB 421 LSENSTFGSGH 431
 RESULT 12
 AAU97741
 XX AAU97741 standard; Protein; 416 AA.
 XX AC AAU97741;
 XX DT 27-AUG-2002 (first entry)
 XX DE Mouse TGR346b polypeptide.
 XX KW Mouse; TGR346b; receptor; G-protein coupled receptor; GPCR; TGR;
 KW TGR-associated disorder; signal transduction; renal failure; nephritis;
 KW hypothyroidism; hypogonadism; retinitis pigmentosa; growth disorder;
 KW diabetes insipidus; hyperprolactinemia; thirst disturbance; appetite;
 KW sleep disturbance; temperature regulation; blood pressure; hypothalamus;
 KW circadian rhythm.
 XX OS Mus sp.
 XX WO200242458-A2.
 XX PD 30-MAY-2002.
 XX PF 21-NOV-2001; 2001WO-US43404.
 XX 22-NOV-2000; 2000US-252841P.
 PR 22-DEC-2000; 2000US-257636P.
 PR 12-JAN-2001; 2001US-261377P.
 PR 28-MAR-2001; 2001US-279554P.
 PR 29-MAR-2001; 2001US-280696P.
 XX (TULA-) TULARIK INC.
 XX Tian H, Zhao J, Chen J, Cutler G, An S, Dai K, Gupte JS;
 XX WPI: 2002-463633/49.
 DR N-PSDB; ABK86293.
 XX New isolated G-protein coupled receptor polypeptide, termed TGR, for
 PT diagnosis and treatment of diseases such as renal failure, nephritis,
 PT hypothyroidism, diabetes insipidus, and disturbances of thirst and
 PT sleep -
 XX
 PS Claim 29; Page 79; 98pp; English.
 CC The invention relates to a G-protein coupled receptor polypeptide (GPCR),
 CC termed TGR, and its associated nucleic acid. The sequences of the
 CC invention are useful for identifying a compound that modulates signal
 CC transduction and for identifying a mammal having a TGR-associated
 CC disorder. The proteins and nucleic acids are useful in diagnosis and
 CC treatment of diseases or conditions such as renal failure, nephritis,
 CC hypothyroidism, hypogonadism, retinitis pigmentosa, growth disorders,
 CC diabetes insipidus, hyperprolactinemia and disturbances of thirst,
 CC sleep, temperature regulation, appetite, blood pressure or any other
 CC syndrome or disease associated with the hypothalamus. The sequences can
 CC be used in regulation of circadian rhythms, for use as genetic markers
 CC for the identification of mutations associated with diseases resulting
 CC from GPCR inactivation in particular cell types and for identification of
 CC modulators of GPCR signal transduction. This sequence represents the
 CC mouse TGR346b polypeptide.
 XX Sequence 416 AA;
 Query Match 79.1%; Score 1767; DB 23; Length 416;
 Best Local Similarity 80.1%; Pred. No. 9.2e-186;
 Matches 339; Conservative 36; Mismatches 38; Indels 10; Gaps 3;
 QY 5 NITPEQFSRLLRDHNLTRQFIYALVRLPLVYTPPELPGRAKLVLVGLVIFALALFNGA 64

OS Rattus norvegicus.
 XX Key Location/Qualifiers
 FH Domain /note= "transmembrane domain I"
 FT Domain 44..71
 FT Domain /note= "transmembrane domain I"
 FT Domain 91..104
 FT Domain /note= "transmembrane domain II"
 FT Domain 123..141
 FT Domain /note= "transmembrane domain III"
 FT Domain 161..180
 FT Domain /note= "transmembrane domain IV"
 FT Domain 220..243
 FT Domain /note= "transmembrane domain V"
 FT Domain 271..296
 FT Domain /note= "transmembrane domain VI"
 FT Domain 314..339
 FT Domain /note= "transmembrane domain VII"
 FT Modified-site 10
 FT Modified-site /note= "N-glycosylated"
 FT Modified-site 18
 FT Modified-site /note= "N-glycosylated"
 FT Modified-site 113
 FT Modified-site /note= "N-glycosylated"
 FT Modified-site 195
 FT Modified-site /note= "N-glycosylated"
 FT Modified-site 154
 FT Modified-site /note= "O-phosphorylated"
 FT Modified-site 263
 FT Modified-site /note= "O-phosphorylated"
 FT Modified-site 264
 FT Modified-site /note= "O-phosphorylated"
 XX
 PN W0200018438-A1.
 XX
 XX 06-APR-2000.
 XX
 XX 24-SEP-1999; 99WO-US22384.
 XX
 XX 25-SEP-1998; 98US-0161113.
 XX 22-FEB-1999; 99US-0255368.
 XX
 XX (SYNA-) SYNAPTIC PHARM CORP.
 XX
 XX Gerald CFG, Jones KA, Bonini JA, Borowsky B;
 XX WPI; 2000-293017/25.
 XX N-PSDB; AAZ94669.
 XX
 XX Nucleic acid encoding a mammalian neuropeptide FF (NPFF) receptor,
 XX useful for treatment of e.g pain, obesity, diabetes, hypertension,
 XX hypotension, hypoglycemia, respiratory disorders
 XX
 XX Claim 21; Fig 23A-B; 253pp; English.
 XX
 XX The present sequence is that of rat neuropeptide FF (NPFF2)
 XX receptor, as deduced from a cDNA clone (see AAZ94669). Isolated
 XX from rat spinal cord cDNA. High levels of rat NPFF2 mRNA are
 XX found in the central nervous system. Expression patterns suggest
 XX roles for NPFF2 in neuroendocrine regulation, and in regulation of
 XX circadian rhythm, regulation of appetite and other functions
 XX modulated by the hypothalamus. A possible role in regulation of
 XX cardiovascular function is also suggested. High levels in the
 XX amygdala suggest a role in modulation of mood, fear, phobia and
 XX anxiety, and NPFF2 may be a target for treatment of depression and
 XX other neuropsychiatric disorders. The invention provides rat
 XX and human NPFF polypeptides and polynucleotides, vectors, host
 XX cells, antibodies, nucleic acid probes, antisense oligonucleotides,
 XX transgenic animals, methods of isolating mammalian NPFF receptors,
 XX methods of treating an abnormality associated with NPFF receptor
 XX activity, methods of determining binding of compounds to NPFF
 XX receptors, methods of identifying agonists and antagonists of NPFF
 XX receptors, and the agonists and antagonists obtained. Claimed
 XX methods of treating an abnormality that is alleviated by

CC increasing/decreasing NPFF activity involve administering an NPFF
 CC receptor agonist/antagonist. The abnormality is a lower urinary
 CC tract disorder, an epinephrine release disorder, a gastrointestinal
 CC disorder, irritable bowel syndrome, a cardiovascular disorder, an
 CC electrolyte balance disorder, diuresis, hypertension, hypotension,
 CC diabetes, hypoglycemia, a respiratory disorder, asthma, a
 CC reproductive function disorder, an immune disorder, an endocrine
 CC disorder, a musculoskeletal disorder, a neuroendocrine disorder, a
 CC cognitive disorder, a memory disorder, a sensory modulation and
 CC transmission disorder, a motor coordination disorder, a sensory
 CC integration disorder, obesity, pain, psychotic behaviour,
 CC morphine tolerance, nicotine addiction, opiate addiction,
 CC affective disorder or migraine (all claimed).
 XX
 XX Sequence 417 AA;
 SQ
 Query Match 22.7%; Score 508; DB 21; Length 417;
 Best Local Similarity 31.8%; Pred. NO. 6.9e-47;
 Matches 119; Conservative 72; Mismatches 145; Indels 38; Gaps 9;
 QY 54 LIPALALFGNALVYVYVTRSKAMRTVTNIFICSLALSDLLITFFCIPVTMLQNISDNWLG 113
 DB 54 LIPFLCMGNTVVCVFIIRNYHTVTNFFIFNLALSDLLVGFICMPITLLDNIAGWPF 113
 QY 114 GAFICKWVPFVQSTAVVTBILTMTCTIAVERHOGLVHPFKMKQYTNRRFTMLGVVWLVA 173
 DB 114 GSSMKISGLVQGISVAASVFTLVAIVDFRCVYVFPK--LTVKTAFAVMIWIWGLA 171
 QY 174 VIVGSP---MHWQQLKIKYDFLYEKH-----ICLEWTSPPVHOKIYTTFILVILFL 224
 DB 172 ITIMTPSAINLHVQ--EEKYVRVLLSHNKTSTVYVWCRDWPNQEMRRIVTTVLFIATYL 229
 QY 225 LPLVMYLLYKIGYELWIKRVDGSLVLTINGKEMSKIAKKKAVIMMYVVALPAV 284
 DB 230 APLSLIVIMYARIGASLFTSAHSTGK-----QRLEQWVHVKKKQKVIKLLTVALLFIL 284
 QY 285 CWAPFVHVHMIEYSNFEKEYDDVTIKMIFAIVQIIGFSNICTNPITYAFMNFKNVL 344
 DB 285 SWLPLWTLMLSDYADLSNKLRLVINIYVYPAHMLAFCSNVNPIIYGFNFNFRSGFQ 344
 QY 345 SAVCYIVNKTSPAQRHNSGITWMRKAKPSLR-----ENPVEETKG-EAFS 392
 DB 345 DAFQFC--OKVKPQEAAG-----LRKRNLIDINTSGLLVHPASQNPSENLGCRKSA 396
 QY 393 DGNIEVKLCQTEE 406
 DB 397 DNPQESLMEETGE 410
 RESULT 15
 AA081358
 ID AA081358 standard; Protein; 420 AA.
 XX
 XX AA081358;
 XX
 XX 30-MAR-1999 (first entry)
 XX
 XX Human 7-transmembrane receptor HLMAR77.
 XX
 XX Human; transmembrane receptor; antagonist; infection; bacterium; fungus;
 XX protozoan; virus; HIV; pain; cancer; anorexia; bulimia; asthma; ulcer;
 XX Parkinson's disease; heart failure; hypotension; hypertension; asthma;
 XX urinary retention; osteoporosis; angina pectoris; myocardial infarction;
 XX allergy; benign prostatic hypertrophy; neurological disorder.
 XX
 XX Homo sapiens.
 XX
 XX EP894387-A2.
 XX
 XX 16-DEC-1998.
 XX
 XX 09-JUN-1998; 98EP-0304580.
 XX

```

PR 13-JAN-1998;      96US-0006140.
PR 11-JUN-1997;    97US-0049332.
PR 02-DEC-1997;    97US-0067253.
XX
XX (SMIK ) SMITHKLINE BEECHAM CORP.
XX
XX Elshourbagy N, Sathe G;
XX
XX MPI; 1999-026581/03.
XX
XX N-PSDB; AAV68484.
XX
XX New DNA encoding 7-trans-membrane receptor polypeptide HLMAR77 -
PT used to treat, diagnose and prevent infections, pain, cancers,
PT anorexia, asthma, Parkinson's disease, acute heart failure,
PT osteoporosis, ulcers, allergies and psychotic disorders
XX
XX Claim 11; Page 8-9; 27pp; English.
XX
XX This sequence represents the human 7-transmembrane receptor HLMAR77.
CC The protein can be used to isolate agonists and antagonists. These can
CC be used as active agents in the treatment of infections (e.g. bacterial,
CC fungal, protozoal and viral infections, particularly HIV-1 or HIV-2),
CC pain, cancers, anorexia, bullmia, asthma, Parkinson's disease, acute
CC heart failure, hypotension, hypertension, urinary retention,
CC osteoporosis, angina pectoris, myocardial infarction, ulcers, asthma,
CC allergies, benign prostatic hypertrophy and psychotic and neurological
CC disorders.
XX
XX Sequence 420 AA;
SQ
Query Match          22.5%; Score 502; DB 20; Length 420;
Best Local Similarity 30.1%; Pred. No.3.2e-46;
Matches 128; Conservative 87; Mismatches 162; Indels 48; Gaps 12;
QY 14 LLRDHNLRTRQFIALRYRLPLVVPPELPGRAKLALVLGTGLFALALFGNALVFVVWTRS 73
DB 26 LYSDDNIT---YNNYYLHQPV-----AAFIISYFLIFFLCMGNTVVCIVVRN 73
QY 74 KAMRTVNIFCSIALSDLLITFFCIPVTMLQNIDSNLWGAFICKMVPFYQSTAVVTEI 133
DB 74 KHWHVTNLFTLNLAISDLLVGICPMETILLDNIAGWPFGNTWKCKISGLVQGIVSVAASV 133
QY 134 LTWTCTAVERHOGHLVHPFKMKQVYNRPFMTLGVWLVAIVIGSP---MHWVOOLEIKY 190
DB 134 FTLVAIADVRFQCVPVYPFKP-K-LTIKTAFVIIMIWLTAITMSPSAVMLHVQE-EKY 190
QY 191 DFLYEKEH-----ICCLEBWTSPVHQKIYTFILVILFLPLMWMLLYSKIGVELWKK 245
DB 191 RVLNSONKTSPPVWCREDPNQEMRKITYTVLFANIYLAPLSLIVIMGIGISLP---- 247
QY 246 RVGDGSVLRTHGKEMSK-----IARKKKRAVINMVTVVALFAVCWAPPHVVHMIMIEYSNF 301
DB 248 ---RAAPEHT--GRKNQEQHWVSRRKQKIKULLIALLFILSWLPLTWLTMLMSDVADL 302
QY 302 EKEYDDYTIRMIPAIVQLIGFSNICHPNVIAFMENPKNVLSAVCYIVNKTFSPAQR 361
DB 303 SPNELQINIITYYTPAHWLAFGNSVNPILIYGFNFENFRRGFQBAFOLQLOCRKAKPMEA 362
QY 362 HGNSGITWMRRKKAFLSRLENPVEETKGEA-FSDGNIEVKLCOEQTBEKKKLKRHLALPRE 420
DB 363 YA-----LKASHVLINTSNQLVQESITFQNEHGHTLLYRKAEKPQDE----LWME 410
QY 421 LAENS 425
DB 411 LKETT 415

```

Search completed: October 28, 2003, 10:12:10
Job time : 89 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 28, 2003, 10:08:34 ; Search time 42 Seconds
(without alignments)
986.874 Million cell updates/sec

Title: US-10-070-241B-1

Perfect score: 2235

Sequence: 1 MQALNITPEQFSRLRDHNL.....RHLALFSELAENSLDSGH 431

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 76:*

1: Piri:*

2: Pir2:*

3: Pir3:*

4: Pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	469.5	21.0	381	2	I39187
2	466.5	20.0	375	2	neuropeptide Y/pep
3	426	19.1	382	2	S27388
4	425.5	19.0	375	2	neuropeptide Y rec
5	425.5	18.0	375	2	pancreatic polypep
6	425.5	19.0	449	2	I39182
7	425	19.0	382	2	neuropeptide Y/pep
8	421.5	18.9	384	2	neuropeptide Y/pep
9	420.5	18.8	349	2	S12863
10	420.5	18.8	349	2	I59336
11	412.5	18.5	366	2	S71152
12	402.5	18.0	427	2	S50150
13	401	17.9	519	2	S17783
14	400.5	17.9	423	2	B40470
15	398	17.8	457	2	T29741
16	386.5	17.3	407	2	S23510
17	384	17.2	402	2	I58595
18	383.5	17.2	407	1	JQ1274
19	382.5	17.1	444	2	A42685
20	381.5	17.1	443	2	D40470
21	379	17.0	428	2	JN0692
22	378.5	16.9	430	2	I51898
23	378	16.9	385	2	SS5524
24	377.5	16.9	423	2	JC7677
25	377.5	16.9	584	2	JC7809
26	375.5	16.8	412	2	T22076
27	375.5	16.8	436	2	JC5599
28	372	16.6	452	2	A34916
29	370.5	16.6	384	2	S20303

30	370.5	16.6	399	2	A46632
31	370.5	16.6	399	2	S29480
32	369	16.5	384	2	I57957
33	367.5	16.4	407	2	A43357
34	367.5	16.4	491	2	C40470
35	366.5	16.4	407	2	S20304
36	365	16.3	398	1	JQ1059
37	364.5	16.3	384	2	I57682
38	362.5	16.2	384	1	S00516
39	362.5	16.2	384	2	A39003
40	362.5	16.2	465	1	JQ1517
41	361	16.2	370	1	I52315
42	360.5	16.1	390	2	B41007
43	359.5	16.1	390	2	A36737
44	359	16.1	384	2	A41007
45	359	16.1	390	2	JH0374

ALIGNMENTS

RESULT 1

I39187

N/Alternate names: neuropeptide YY receptor Y2 - human

C/Species: Homo sapiens (man)

C/Date: 01-Mar-1996 #sequence revision 01-Mar-1996 #text_change 20-Apr-2000

C/Accession: I39187; I39163; G02301

R/Gerald, C.; Walker, M.W.; Vayssie, P.J.

J. Biol. Chem. 270, 26758-26761, 1995

A/Title: Expression cloning and pharmacological characterization of a human hippocampal

A/Reference number: I39187; MUID:96070760; PMID:7592910

A/Accession: I39187

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-381 <GER>

A/Cross-references: EMBL:U36269; NID:G1063633; PIDN:AA050281.1; PID:G1063634

R/Rose, P.M.; Fernandes, P.; Lynch, J.S.; Frazier, S.T.; Fisher, S.M.; Kodukula, K.; Kie

J. Biol. Chem. 270, 22661-22664, 1995

A/Title: Cloning and functional expression of a cDNA encoding a human type 2 neuropeptic

A/Reference number: I39183; MUID:96032678; PMID:7559383

A/Accession: I39163

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-133 'A', 135-381 <ROS>

A/Cross-references: EMBL:U32500; NID:G1000750; PIDN:AAA93170.1; PID:G1000751

R/Yan, H.; Yang, J.; Marasco, J.; Yamaguchi, K.; Brenner, S.; Collins, F.; Karbon, W.

submitted to the EMBL Data Library, December 1995

A/Reference number: H01019

A/Accession: G02301

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-171 'G', 173 'R', 175-201 'P', 203-208 'A', 210-381 <YAN>

A/Cross-references: EMBL:U42389; NID:G1314329; PIDN:AA07760.1; PID:G1314330

C/Genetics:

A/Gene: GDB:NPY2R

A/Cross-references: GDB:4365607; OMIM:162642

A/Map position: 4q31-4q31

C/Superfamily: neurokinin 1 receptor

C/Keywords: appetite; G protein-coupled receptor; glycoprotein; lipoprotein; thiolester

F:49-76/Domain: transmembrane #status predicted <TM1>

F:166-186/Domain: transmembrane #status predicted <TM2>

F:221-237/Domain: transmembrane #status predicted <TM3>

F:269-291/Domain: transmembrane #status predicted <TM4>

F:305-328/Domain: transmembrane #status predicted <TM5>

F:123-203/Disulfide bonds: #status predicted <TM6>

F:372/Binding site: palmitate (Cys) (covalent) #status predicted

F:372/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match

Best Local Similarity 21.0%; Score 469.5; DB 2; Length 381;

Matches 113; Conservative 75; Mismatches 123; Indels 53; Gaps 13;

QY 7 TPEQFSLRLDRHNLTRQFIALYRLRLVYTPPELPGRAKALALVLTGVLIFALALFGNALV 66
DB 26 TPNFSEHCQSDVDVMVFIVTSISITVV-----GVL-----GNLCL 62
QY 67 FYVVTGRKAMRTVTNIFICSLALSDLLITFFCIPVTMLQNSINWLGGAFCIKMVPFVQS 126
DB 63 MCVTVRQEKANVTNLIANAFSDFLWCLLCQPLTSVITMDYIFGETLCKNSAFIQ 122
QY 127 TAVVTEILTWTCTIAVERHQGLVHPFKMKQYTNERRAFTMLGVVWLAVVGVSPMWHVQOL 186
DB 123 MSVTVSILSLVALERHQLIINF--TGWKPSISQAYLGVLIVLWVAVLWVPLFANSIL 180
QY 187 EIKY-----DFLYEKEHCCLLEWTSVPHQKIYTTFTILVILFLPLMVMILYKIG 238
DB 181 ENVFHKNHSALEFLADK--VVTESPLAHHTIYTTFLLLFOYCLPLGLFVLCVARIY 238
QY 239 YELMIKKRVGDSGLVLTTHGKEMSKIARKKRAVIMVTVVALFVCAWPHFVHVMIEY 298
DB 239 RRL---QROG-----RVFHKGTYSLRAGHKMQVNVVWVAVFVWVAVLPLHVFNSLEDW 290
QY 299 SNPEKEYDDVTI---KMFPAIVQIIGFSNSICNPVIVAFNMENFKKNVLSAVCYCIVNKT 355
DB 291 -----HHEAIPICHGNLIFLVCHLLAMASTCVNPFYIFLNTFNFKKEIKALVLTQOOSAP 345
QY 356 PSPAQRHNGSGI--TMMRKKAFTSLRNPV 383
DB 346 LESEHPLSTVHTVTEVSKGSLRSGRSNPI 375

RESULT 5
I39182
neuropeptide Y/peptide YY receptor Y4 - human
C;Species: Homo sapiens (man)
C;Date: 01-Mar-1996 #sequence_revision 01-Mar-1996 #text_change 20-Apr-2000
C;Accession: I39182
R;Bard, J.A.; Walker, M.W.; Branchek, T.A.; Weinshank, R.L.
J. Biol. Chem. 270, 26762-26765, 1995
A;Title: Cloning and functional expression of a human Y4 subtype receptor for pancreatic
A;Reference number: I39182; MUID:96070761; PMID:7592911
A;Accession: I39182
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-375 <RES>
A;Cross-references: EMBL:U35232; NID:g1063629; PIDN:AAC50280.1; PID:g1063630
C;Superfamily: neurokinin 1 receptor
C;Keywords: appetite

Query Match 19.0%; Score 425.5; DB 2; Length 375;
Best Local Similarity 27.4%; Pred. No. 6.5e-27;
Matches 107; Conservative 76; Mismatches 154; Indels 53; Gaps 10;

QY 7 TPEQFSLRLDRHNLTRQFIALYRLRLVYTPPELPGRAKALALVLTGVLIFALALFGNALV 66
DB 26 TPNFSEHCQSDVDVMVFIVTSISITVV-----GVL-----GNLCL 62
QY 67 FYVVTGRKAMRTVTNIFICSLALSDLLITFFCIPVTMLQNSINWLGGAFCIKMVPFVQS 126
DB 63 MCVTVRQEKANVTNLIANAFSDFLWCLLCQPLTSVITMDYIFGETLCKNSAFIQ 122
QY 127 TAVVTEILTWTCTIAVERHQGLVHPFKMKQYTNERRAFTMLGVVWLAVVGVSPMWHVQOL 186
DB 123 MSVTVSILSLVALERHQLIINF--TGWKPSISQAYLGVLIVLWVAVLWVPLFANSIL 180
QY 187 EIKY-----DFLYEKEHCCLLEWTSVPHQKIYTTFTILVILFLPLMVMILYKIG 238
DB 181 ENVFHKNHSALEFLADK--VVTESPLAHHTIYTTFLLLFOYCLPLGLFVLCVARIY 238
QY 239 YELMIKKRVGDSGLVLTTHGKEMSKIARKKRAVIMVTVVALFVCAWPHFVHVMIEY 298
DB 239 RRL---QROG-----RVFHKGTYSLRAGHKMQVNVVWVAVFVWVAVLPLHVFNSLEDW 290
QY 299 SNPEKEYDDVTI---KMFPAIVQIIGFSNSICNPVIVAFNMENFKKNVLSAVCYCIVNKT 355

DB 291 -----HHEAIPICHGNLIFLVCHLLAMASTCVNPFYIFLNTFNFKKEIKALVLTQOOSAP 345
QY 356 PSPAQRHNGSGI--TMMRKKAFTSLRNPV 383
DB 346 LESEHPLSTVHTVTEVSKGSLRSGRSNPI 375

RESULT 6
A41738
neuropeptide Y receptor - fruit fly (Drosophila melanogaster)
N;Alternate names: G protein-coupled receptor PR4
C;Species: Drosophila melanogaster
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 20-Apr-2000
C;Accession: A41738
R;Li, X.J.; Wu, Y.N.; North, R.A.; Forte, M.
J. Biol. Chem. 267, 9-12, 1992
A;Title: Cloning, functional expression, and developmental regulation of a neuropeptide
A;Reference number: A41738; MUID:92112730; PMID:1370455
A;Molecule type: mRNA
A;Residues: 1-449 <LIA>
A;Cross-references: GB:M81490; NID:g157996; PIDN:AAA28727.1; PID:g157997
C;Genetics:
A;Gene: FlyBase:NepYr
A;Cross-references: FlyBase:FBgn0004842
C;Superfamily: neurokinin 1 receptor
C;Keywords: appetite; G protein-coupled receptor; transmembrane protein

Query Match 19.0%; Score 425.5; DB 2; Length 449;
Best Local Similarity 28.4%; Pred. No. 7.9e-27;
Matches 111; Conservative 74; Mismatches 157; Indels 49; Gaps 12;

QY 17 DHNLTRQFIALYRLRLVYTPPELPGRAKALALVLTGVLIFALALFGNALVYVVTGRSKAM 76
DB 75 DDLLSEDMWSSAYFKIIVMLYIP-----IFPALINGVTVCYIVYTFPM 121
QY 77 RTVTNIFICSLALSDLLITFFCIPVTMLQ--NIDSNWLGGAFCIKMVPFVQSTAVVTEILT 135
DB 122 RTVTNFIASLAIGDILMSFFCEPSSFISLILNWPFGGLALCHFPVNSQAVSLVSAYT 181
QY 136 MTCIAVERHQGLVHPFKMKQYTNERRAFTMLGVVWLAVVGVSPMWHVQOLEIKYDFLYE 195
DB 182 LVAISIDRYAIAMWPLKPR--ITKRYATFIAGWFIATATLPIPIVSGLDIPNGFWHT 239
QY 196 K-EHICCLEWTSVPHQKIYTTFTILVILFLPLMVMILYKIGYBELWIKKRVGDSGLR 254
DB 240 KCEYICREWMPSPRSQEQYYTTLSELFALQFVPLGVILFYARITIRVWAKRPGEAETNR 299
QY 255 TIHGKEMSKIARKKRAVIMVTVVALFVCAWPHFVHVMIEYSNPEKEYDDVTIKMIF 314
DB 300 D-----QRMARSKRKMKMLTWTIVFTCCMLPFNLQLLLNDEBP-AHWD--PLEYVW 350
QY 315 AIYQIIGFSNSICNPVIVAFNMENFKKNVLSAV-----CYCI-----VKNKTF-- 357
DB 351 FAFNLAMSHCCYNPPIIYCYNNARFRSGFVQLMHRMPGLRW-CLSVGDNRNATSGTG 409
QY 358 ---PAQRHNGSG--ITMRRKKAFTSLRNPV 383
DB 410 PALPLANMTSTTYISARRKPRATSLRANPL 440

RESULT 7
B46133
neuropeptide Y/peptide YY receptor Y1 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 20-Apr-2000
C;Accession: B46133
R;Herzog, H.; Hort, Y.J.; Ball, H.J.; Hayes, G.; Shine, J.; Selbie, L.A.
Proc. Natl. Acad. Sci. U.S.A. 89, 5794-5798, 1992
A;Title: Cloned human neuropeptide Y receptor couples to two different second messenger
A;Reference number: A46133; MUID:92335184; PMID:1321422
A;Accession: B46133
A;Status: preliminary; not compared with conceptual translation

A:Molecule type: nucleic acid

A:Residues: 1-382 <HER>

A>Note: sequence extracted from NCBI backbone (NCBIP:108539)

C:Superfamily: neurokinin 1 receptor

C:Keywords: appetite; G protein-coupled receptor; transmembrane protein

Query Match 19.0%; Score 425; DB 2; Length 382;
Best Local Similarity 28.6%; Pred. No. 7.3e-27;
Matches 106; Conservative 71; Mismatches 126; Indels 68; Gaps 12;

QY 46 LALVLTGVLTFALALFGNALVFYVTRSKAMRTVTNIFICSLALSDLLITPFCIPVTLQ 105

DB 42 LALAYGVII--LGVSGNLALIIIIKQKERNVTNIIIVNLSFSLVAVMCLPFTFY 99

QY 106 NISDNMLGGAFICKMVPFVOSTAVTEILTMTCIAVERHOGVLHPFKMKQVTRRAFTM 165

DB 100 TLMDSHWVFGTECKLPNFVQCVSITVPSLVLIAVERHQLINP--RGWRNNRHAYIG 157

QY 166 LGVVLVAVIVGSPMHHVQQLTKYDFLYE-----KEHICCLEBEWTSVPHQKIY 214

DB 158 ITVIWLVAVASSLPF-----VIYQILDEPPQNVSLAFAFKDKYVCFDKFSDSHRLSY 210

QY 215 TTPILVILFLPLMVLMLIYKIGYELWIKRVGDSGLVLRTHGKEMSKIARKK----- 268

DB 211 TLLLVLYQFGPLCFIFCYKIVIRL--KRR-----NNMKDKIRSKYRSSET 257

QY 269 KRAVIMVTVVAVFACVWAP---PHVV---HMMIYSNFEKEYDDVTIKMFAIVQIIG 321

DB 258 KRINWMLLSIVVAVACVWLPITFTNTVFDNHHQIATCNH-----NLLFLCHLTAM 308

QY 322 FSNICNPPIVYAPMENEFKNVLSAVCYCIVN-----KTFSPAQRHNGSGITMRKKA- 374

DB 309 MISTCVNPIFYGLNKNFQDLQFFNFCDFRSDDDYETIAMSTWHTDVSNTLSLKQASP 368

QY 375 ----KPSLRN 381

DB 369 VAFKKISMNDN 379

RESULT 8

A45490

neuropeptide Y/peptide YY receptor Y1 - human

C:Species: Homo sapiens (man)

C>Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 20-Apr-2000

C:Accession: A45490; A46133; A42773

R:Herzog, H.; Baumgartner, M.; Vivero, C.; Selbie, L.A.; Auer, B.; Shine, J.

J. Biol. Chem. 268, 6703-6707, 1993

A>Title: Genomic organization, localization, and allelic differences in the gene for the

A:Reference number: A45490; MUID:93203272; PMID:8095935

A:Accession: A45490

A:Molecule type: DNA

A:Residues: 1-384 <HER>

A:Cross-references: GB:L07615; NID:g189284; PIDN:AAA59947.1; PID:g189285

A>Note: sequence extracted from NCBI backbone (NCBIP:128005, NCBIP:128000)

R:Herzog, H.; Hott, Y.J.; Ball, H.J.; Hayes, G.; Shine, J.; Selbie, L.A.

Proc. Natl. Acad. Sci. U.S.A. 89, 5794-5798, 1992

A>Title: Cloned human neuropeptide Y receptor couples to two different second messenger

A:Reference number: A46133; MUID:92335184; PMID:13121422

A:Accession: A46133

A>Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-384 <HER2>

A>Note: sequence extracted from NCBI backbone (NCBIP:108538)

R:Arhammar, D.; Blomqvist, A.G.; Yee, F.; Jazin, E.; Yoo, H.; Wahlested, C.

J. Biol. Chem. 267, 10935-10938, 1992

A>Title: Cloning and functional expression of a human neuropeptide Y/peptide YY receptor

A:Reference number: A42773; MUID:92283782; PMID:1317848

A:Accession: A42773

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-384 <LAR>

A:Cross-references: GB:M88461; NID:g189155; PIDN:AAA73215.1; PID:g189156

A:Experimental source: fetal brain

A>Note: sequence extracted from NCBI backbone (NCBIP:104735, NCBIP:104736)

C:Genetics:

A:Gene: GDB:NPY1R; NPYR

A:Cross-references: GDB:132643; OMIM:162641

A:Map position: q31.3-q32

C:Superfamily: neurokinin 1 receptor

C:Keywords: appetite; G protein-coupled receptor; glycoprotein; lipoprotein; thiolester

F:37-66/Domain: transmembrane #status predicted <TM1>

F:77-103/Domain: transmembrane #status predicted <TM2>

F:118-136/Domain: transmembrane #status predicted <TM3>

F:155-179/Domain: transmembrane #status predicted <TM4>

F:209-232/Domain: transmembrane #status predicted <TM5>

F:261-286/Domain: transmembrane #status predicted <TM6>

F:300-323/Domain: transmembrane #status predicted <TM7>

F:113-198/Disulfide bonds: #status predicted

F:186/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:338/Binding site: palmitate (Cys) (covalent) #status predicted

Query Match 18.9%; Score 421.5; DB 2; Length 384;

Best Local Similarity 30.2%; Pred. No. 1.4e-26;

Matches 99; Conservative 66; Mismatches 114; Indels 49; Gaps 11;

QY 46 LALVLTGVL-----IFALALFGNALVFYVTRSKAMRTVTNIFICSLALSDLLITPFCIPV 101

DB 37 LAMIFTLALAYGAVIILGVSGNLALIIIIKQKERNVTNIIIVNLSFSLVAVMCLPFP 96

QY 102 TMLONISDNMLGGAFICKMVPFVOSTAVTEILTMTCIAVERHOGVLHPFKMKQVTRNR 161

DB 97 TFFVTLMDSHWVFGTECKLPNFVQCVSITVPSLVLIAVERHQLINP--RGWRNNRH 154

QY 162 AFTMLGVVVLVAVIVGSPMHHVQQL-----ETKYDFLYEKEHICCLEBEWTSVPHQKIY 215

DB 155 AYVGIAVIWLVAVASSLPFTIYQVMTDEPPQNVTLQ-AYKDKYV-CFDQFPSPSHLSYT 212

QY 216 TFLVILFLPLMVLMLIYKIGYELWIKRVGDSGLVLRTHGKEMSKIARKK-----K 269

DB 213 TLLLVLYQFGPLCFIFCYKIVIRL--KRR-----NNMKDKIRSKYRSSETK 259

QY 270 RAVIMVTVVAVFACVWAP---PHVV---HMMIYSNFEKEYDDVTIKMFAIVQIIGF 322

DB 260 RINIMLSIVVAVACVWLPITFTNTVFDNHHQIATCNH-----NLLFLCHLTAM 310

QY 323 SNSTCNPIVYAPMENEFKNVLSAVCYC 350

DB 311 ISTCVNPIFYGLNKNFQDLQFFNFPC 338

RESULT 9

S12863

G protein-coupled receptor PC5 - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 20-Apr-2000

C:Accession: S12863; S19101

R:Eva, C.; Keinänen, K.; Mönner, H.; Seeburg, P.; Sprengel, R.

FEBS Lett. 271, 81-84, 1990

A>Title: Molecular cloning of a novel G protein-coupled receptor that may belong to the

A:Reference number: S12863; MUID:91032093; PMID:2172008

A:Accession: S12863

A:Molecule type: mRNA

A:Residues: 1-349 <EVA>

A:Cross-references: EMBL:Z11504

R:Krause, J.; Eva, C.; Seeburg, P.; Sprengel, R.

submitted to the EMBL Data Library, November 1991

A:Description: Pharmacological and Transduction Properties of a Recombinantly Expressed

A:Reference number: S19101

A:Accession: S19101

A:Molecule type: mRNA

A:Residues: 1-343 'DDYETIAMSTWHTDVSNTLSKQASVPAFKKISMNDNEKI' <KRA>

A:Cross-references: EMBL:Z11504; NID:g57636; PIDN:CAA77579.1; PID:g57637

C:Superfamily: neurokinin 1 receptor

C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane prc

F:39-61/Domain: transmembrane #status predicted <TM1>

F:73-93/Domain: transmembrane #status predicted <TM2>

F:114-135/Domain: transmembrane #status predicted <TM3>
 F:155-175/Domain: transmembrane #status predicted <TM4>
 F:213-231/Domain: transmembrane #status predicted <TM5>
 F:262-285/Domain: transmembrane #status predicted <TM6>
 F:299-322/Domain: transmembrane #status predicted <TM7>
 F:2,11,17/Binding site: carbonyl site (Asn) (covalent) #status predicted
 F:346/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match 18.8%; Score 420.5; DB 2; Length 349;
 Best Local Similarity 30.4%; Pred. No. 1.5e-26;
 Matches 100; Conservative 61; Mismatches 111; Indels 57; Gaps 10;
 QY 46 LALVLTGVLIFALFAGNALVYVYVTRSKAMRTVNTNIFICSALSDLLITFFCIPVMTQ 105
 DB 42 LALAYGAVII--LGVSGLALIIILKOKENAVNTNIIIVNLSFSDLLVAVMCLPPTFVY 99
 QY 106 NISNWLGGAFCKMVPVQSTAVVTEILTWCIAVERHOGVLHPFKMKQYTNRRFTM 165
 DB 100 TLMDEHWFGETMCKLNPVQCVSITVSIFSLVIAVERHQLIINP--RGMWRPNRHAYIG 157
 QY 166 LGVWLVAVIVGSPMWHVQOOLEIKYDFLYE-----KEHICCLEEWTSPVHCKIY 214
 DB 158 ITVIMLVAVASLPP-----VYQILTDEPPQNVSLAAPKDKYVCFDPSPDSHRLSY 210
 QY 215 TTFILVILFLPLMVLILYKIGYELWIKRVDGSGVLRTHGKEMSKIARKK-----268
 DB 211 TTLLVLQVFGCLCFICYFKIYRL--KAR-----NNMMDKIRDSKYRSSET 257
 QY 269 KEAVTMVTVVAFVACVAP---FHVV---HMMIEYSNFEKEDDVTIKMIFAVIOLIG 321
 DB 258 KRINVMLLSIVVAFVACVLPITFTNVDNWHQIATCNH-----NLLFLCLHLTA 308
 QY 322 FSNISICNPIVAFNMENFKKNVLSAVCYC 350
 DB 309 MISTCVNPIFYGLFNKNFQRLQPFENEC 337

RESULT 10

I59336
 galanin receptor 1 - human
 C:Species: Homo sapiens (man)
 C>Date: 31-May-1996 #sequence revision 31-May-1996 #text_change 21-Jul-2000
 C:Accession: I59336; JCS801; G02528
 R:Haabert-Ortoli, E.; Amisano, B.; Loquet, I.; Laburthe, M.; Mayaux, J.
 Proc. Natl. Acad. Sci. U.S.A. 91, 9780-9783, 1994
 A>Title: Molecular cloning of a functional human galanin receptor.
 A:Reference number: I59336; MUID:95024044; PMID:7524088
 A:Accession: I59336
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-349 <HAB>
 A:Cross-references: GB:IJ34339; NID:9559047; PIDN:AAA50767.1; PID:9559048
 R:Loximer, D.D.; Matkowski, K.; Benya, R.V.
 Biochem. Biophys. Res. Commun. 241, 558-564, 1997
 A>Title: Cloning, chromosomal location, and transcriptional regulation of the human galanin receptor.
 A:Reference number: JCS801; MUID:98086390; PMID:9425310
 A:Accession: JCS801
 A>Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-349 <LOR>
 A:Cross-references: GB:U53511; NID:g1297337; PIDN:AAC51936.1; PID:g1297338
 A>Note: submitted to the EMBL Data Library, April 1996
 R:Ross, P.C.
 Submitted to the EMBL Data Library, March 1995
 A:Reference number: G08350
 A:Accession: G01765
 A>Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-14 'W' 16-349 <ROS>
 A:Cross-references: EMBL:U23654; NID:g775209; PID:g775210
 C:Comment: This receptor inhibits cAMP formation, stimulates and inhibits phospholipase C, and increases arachadonic acid metabolism, as well as opens ATP-dependent K+ but close C:Genetics:

A:Gene: GDB:GALNR
 A:Cross-references: GDB:392699; OMIM:600377
 A:Map position: 18q23-18q23
 C:Superfamily: vertebrate rhodopsin

Query Match 18.8%; Score 420.5; DB 2; Length 349;
 Best Local Similarity 32.4%; Pred. No. 1.5e-26;
 Matches 103; Conservative 60; Mismatches 118; Indels 37; Gaps 11;
 QY 46 LALVLTGVLIFALFAGNALVYVYVTRSK--AMRTVNTNIFICSALSDLLITFFCIPVMT 103
 DB 35 VTLVWFG-LIFALGVLGNSLVTILARSKPGKPRSTTNLFILNLSIADLAVLLFCIPQA 93
 QY 104 LONISDNWLGAFICKMVPVQSTAVVTEILTWCIAVERHOGVLHPFKMKQYTNREAF 163
 DB 94 TYVALPTWLGAFICKFIHYFTVSMVLSIFFLAAMSVDRIAVIHSRRSSLSLRVRNAL 153
 QY 164 TMLGVWLVAVIVGSPMWHVQOOLEIKYDFLYE--EHCICCLEEWTSPVHCKIYTTFILVI 221
 DB 154 LGVGCIALWALSIAVASPVAYHQL-----FHPRASNQITFCWEQWDPDRKKAYVCTFVF 207
 QY 222 LFLLPLMVLILYKIGYELWIKRVDGSGVLRTHG--KEMSK--IARKKRAVIMMVT 277
 DB 208 GYLLPLLLLCFCYAK-----VLNHLHKKLKNMSKSEASKKTAQTALV- 251
 QY 278 VVALFAVCWAPVHVHMMIEYSNFEKEDDVTIKMIFAI-VQIIGFSNSICNPIVAFNM 336
 DB 252 VVVVFGISGLWPHIHLWAEFGVFP-----TPASFLFRITAHCLAYSNSVNPILVAFLS 307
 QY 337 ENFKKNVLSAVCYCIVNK 354
 DB 308 ENFRK-AYKQVFKCHIRK 324

RESULT 11

S71152
 neuropeptide Y/peptide YY receptor Y1 - African clawed frog
 C:Species: Xenopus laevis (African clawed frog)
 C>Date: 27-Oct-1996 #sequence revision 13-Mar-1997 #text_change 20-Apr-2000
 C:Accession: S71152; S55924
 R:Marrens, G.J.; Blomqvist, A.G.; Roubos, E.W.; Larhammar, D.
 submitted to the EMBL Data Library, November 1993
 A:Description: Cloning and sequencing of an neuropeptide Y/peptide YY receptor from Xenopus laevis.
 A:Reference number: S71152
 A:Accession: S71152
 A:Molecule type: mRNA
 A:Residues: 1-366 <MAR>
 A:Cross-references: EMBL:L25416; NID:9409169; PIDN:AAA49918.1; PID:g409170
 A:Experimental source: brain, hypothalamus
 R:Blomqvist, A.G.; Roubos, E.W.; Larhammar, D.; Martens, G.J.M.
 Biochim. Biophys. Acta 1261, 439-441, 1995
 A>Title: Cloning and sequence analysis of a neuropeptide Y/peptide YY receptor Y1 cDNA
 A:Reference number: S55924; MUID:95260870; PMID:7742373
 A:Accession: S55924
 A>Status: preliminary; nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-278 'T' 280-366 <BLO>
 A:Cross-references: EMBL:L25416; NID:9409169
 C:Superfamily: neurokinin 1 receptor
 C:Keywords: G protein-coupled receptor; transmembrane protein
 Query Match 18.5%; Score 412.5; DB 2; Length 366;
 Best Local Similarity 29.1%; Pred. No. 7.2e-26;
 Matches 96; Conservative 71; Mismatches 122; Indels 41; Gaps 9;
 QY 33 PLVYTPLEPGRALALVLTGVLIFALFAGNALVYVYVTRSKAMRTVNTNIFICSALSD 92
 DB 33 PMIFT-----LALAYGAVII--LGLSGLNALIIILKOKENAVNTNIIIVNLSFSD 82
 QY 93 LITFFCIPVMTLQNSDNLWLGAFICKMVPVQSTAVVTEILTWCIAVERHOGVLHPFK 152
 DB 83 LATIMCLPTLIYTMDEHWFGEVNMCKLNEYTCQSVTSVIFSLVLIATIERHQLIINP-- 140

QY	153	MKWQYTNRRFTMLGVVWLVAVVIGSPMMHVQQL-----EIKYDPLYEKEHICCLEEWT	208
Db	141	RGWRPNRRHACFGITVINGFAMACSTPLMWYSVLITDPEFKNISLDSVIGK--YVCLEDFP	198
QY	207	SPVHOKIYTFILVILFLLPLAVMLILYSKIGYELWIKRVGDSGLVRIIHKEMSKIAR	266
Db	199	EDKFLSYTTLFILOYLGLPCLFVICYTKI--FURLKER-----NNMMDKIRD	245
QY	267	KK-----KRAVIMVTVVVALFVACWAPPHVMMIEYISNFKEYDDVTIKMIFAIVQII	320
Db	246	NKYRSSETKRINIMLLSIUVGFALCWLPPFIINLVFDWNH--EAVATCNHNLFLICHT	303
QY	321	GFSNSICNPIVYAFMNEFKKIVLSAVCYC	350
Db	304	AMISCVAPIFYGLFNKNFQDLQPFNFNC	333

RESULT 12
 S50150
 gastric CCK-A receptor - rabbit
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C>Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 20-Apr-2000
 C:Accession: S50150
 R:Reuben, M.; Rising, L.; Prinz, C.; Hersey, S.; Sachs, G.
 Biochim. Biophys. Acta 1219, 321-327, 1994
 A:Title: Cloning and expression of the rabbit gastric CCK-A receptor.
 A:Reference number: S50150; MUID:95002144; PMID:7918628
 A:Accession: S50150
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-427 <REU>
 C:Superfamily: neurokinin 1 receptor

Query Match	18.0%;	Score	402.5;	DB 2;	Length	427;			
Best Local Similarity	27.0%;	Pred. No.	5.5e-25;						
Matches	95;	Conservative	72;	Mismatches	126;	Indels	59;	Gaps	7;

QY	49	VLTVLIPALAFGNALFVYVVTRSKARTVNIIFICSIALSDLLITFCPIPTVMQNIS	108
Db	45	ILLYSLFLLSVLGNLTAVITLIRNKNRTVNIIFLLSLAISDLMLCLPCHPFLNIPNL	104
QY	109	DNWLGGAFCIKMVPFVOSTAVTEILNWTCTIAVERHQGLHPFKMK-WOYTNRRFTMLG	167
Db	105	KDFIFGALCKTITTYLGMTSVSVSTNLVAISLERYGAICKPLQSRVWQ-TKSHALKVIA	163
QY	168	VWMLVAVVIGSPMMHVQQLKYDPLYEKEHICCLEEWTSPVHQIYTFILVILFLLPL	227
Db	164	ATWCLSAIMTP-YPIYENLVFPYTKTNQTNAMCRFLPSDVWQAMHTFLLILFLIPG	222
QY	228	MMMLILYSKIGYELW-----IKKRV-----	247
Db	223	IVMMVAYMISLELYQGIKFDAQSKKAKERKASTGSGRPFEDNDGCVLQSRKPTRQLELQ	282
QY	248	---GDGSLVRIITHGKEMSKIARKKKKAVIMVTVVVALFVACWAPPHVMMIEYISNPEK	303
Db	283	QLSGGGGGRVSRIHSSSSAALMAKKRVIRMLMIVLVLFLLCWMP-----IFSANAWR	335
QY	304	EYDDVTIK-----MIFAIVQIIGFSNICNPIVYAFMNEFKKIVLSAVCYC	350
Db	336	AYDVTSAERLLSGTFPIFILLSYTSSCVNPIIYCFMKNRFLGFMATFPCC	387

RESULT 13
 S17783
 tachykinin receptor homolog DTKR - fruit fly (Drosophila melanogaster)
 C:Species: Drosophila melanogaster
 C>Date: 22-Nov-1996 #sequence_revision 22-Nov-1996 #text_change 20-Apr-2000
 C:Accession: S17783
 R:Li, X.J.; Wolfgang, W.; Wu, Y.N.; North, R.A.; Forte, M.
 EMBO J. 10, 3221-3229, 1991
 A:Title: Cloning, heterologous expression and developmental regulation of a Dro
 A:Reference number: S17783; MUID:9200772; PMID:1717263
 A:Accession: S17783

Result No.	Query			ID	Description
	Score	Match	Length		
1	508	22.7	417	1	NFF2 RAT
2	502	22.5	522	1	NFF2 HUMAN
3	469.5	21.0	381	1	NY2R HUMAN
4	468.5	21.0	381	1	NY2R WACMU
5	467.5	20.9	382	1	NY2R PIG
6	467	20.9	384	1	NY2R BOVIN
7	466.5	20.9	385	1	NY2R MOUSE
8	460.5	20.6	460	1	OX2R MOUSE
9	459.5	20.6	460	1	OX2R RAT
10	457	20.4	381	1	NY2R CAVPO
11	455	20.4	444	1	OX2R HUMAN
12	451	20.2	444	1	OX2R CANFA
13	446.5	20.0	375	1	NY4R MOUSE
14	446	20.0	371	1	NY6R RABIT
15	440	19.7	385	1	NY6R CHICK
16	437	19.6	432	1	NFL1 RAT
17	432.5	19.4	430	1	NFL1 HUMAN
18	431.5	19.3	346	1	GAUR RAT
19	431	19.3	383	1	NY1R CAVPO
20	430.5	19.3	348	1	GAUR MOUSE
21	430.5	19.3	375	1	NY4R RAT
22	429	19.2	371	1	NY6R MOUSE
23	426	19.1	382	1	NY1R MOUSE
24	425.5	19.0	375	1	NY1R HUMAN
25	425.5	19.0	449	1	NY1R DROME
26	425	19.0	382	1	NY1R RAT
27	424	19.0	383	1	NY1R PIG
28	423.5	18.9	382	1	NY1R CANFA
29	422.5	18.9	425	1	OX1R HUMAN
30	421.5	18.9	384	1	NY1R HUMAN
31	420.5	18.8	349	1	GAUR HUMAN
32	412.5	18.5	366	1	NY1R XENLA
33	412.5	18.5	416	1	OX1R RAT

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FT DOMAIN 67 82 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 83 103 2 (POTENTIAL).
FT DOMAIN 104 119 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 120 140 3 (POTENTIAL).
FT DOMAIN 141 160 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 161 181 4 (POTENTIAL).
FT DOMAIN 182 217 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 218 238 5 (POTENTIAL).
FT DOMAIN 239 274 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 275 295 6 (POTENTIAL).
FT DOMAIN 296 310 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 311 331 7 (POTENTIAL).
FT DOMAIN 332 417 CYTOPLASMIC (POTENTIAL).
FT DISULFID 118 206 BY SIMILARITY.
FT CARBOHYD 8 8 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 20 20 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 31 31 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 417 AA; 47710 MW; DFE6AC63AP2AAD6 CRC64;

Query Match 22.7%; Score 508; DB 1; Length 417;
Best Local Similarity 31.8%; Pred. No. 7.5e-29;
Matches 119; Conservative 72; Mismatches 145; Indels 38; Gaps 9;

.QY 54 LIFALALFGNALFYVVTSSKAMRTVTFICSLALSDLIITFFCIPVTMLQMSIDNWLG 113
Db 54 LIFELCWGNVTVCVIRNRYMHTVTFEINLALSDLLVIGFCMPITLLDNIAGWPF 113

.QY 114 GAFICMVPVQSTAVTEILTWCIAVERHQGLVHPFKQVYTNRRFTMLGVVWLVA 173
Db 114 GSMCKISGIVQISVAASFTLVAIVDFRCVYFPFK--LTVKTAFTVMIVVIGLA 171

.QY 174 VIVGSP---NMHWQOOLEIKYDFLYEKH-----ICLEWTSVPVHOKITTTFILVILFL 224
Db 172 ITIWTSAIMLHVQ--BEKYRVYELSHNKTSTVYWCREDWPNQENRYITTVLTAIYL 229

.QY 225 LPLMWMILLYSKYGLWIKKRVGDSVLTTHGKEMSKIARKKRAVIMVTVVALLPAV 284
Db 230 APLSLIVMYARIGASLFTSAHSTGK-----QRLQWHSVKKQKQVIKOLLTVALLFTL 284

.QY 285 CWAPFHVHMIMVSNPEKEDVDVTIKMFAIVQIIGFNSICNPVYAFNMENFKQVNL 344
Db 285 SWLPLTLMLSYADLSFNKLIVINIVYVFAHMLAFNCSSVNPVLIYGFNFNRSFQ 344

.QY 345 SAVCYCIVNKTFFPAQRHSGNITMKKXAKFSLR-----ENPVETKG-EAPS 392
Db 345 DAFQFC--QKVKPQRAYG-----LRAKNLDINTSGLLVHBPASQNSGENLGRCKSA 396

.QY 393 DGNIEVKLCBOTEE 406
Db 397 DNPQESLMEETGE 410

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RESULT 2

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NEF2 HUMAN
ID NEF2 HUMAN STANDARD; PRT; 522 AA.
AC Q9YX53; Q96RV1; Q9NR49;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Neuropeptide FF receptor 2 (Neuropeptide G protein-coupled receptor)
DE (G-protein-coupled receptor HLWAR77).
GN GPR74 OR NPGPR OR NPF2.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A. (ISOFORM 1), AND TISSUE SPECIFICITY.
RC TISSUE=Fetal.
PX MEDLINE=99180505; PubMed=10079187;
RA Ciklos S., Gregor P., Koppal J.;
RT "Sequence and tissue distribution of a novel G-protein-coupled

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receptor expressed prominently in human placenta.";
Biochem. Biophys. Res. Commun. 256:352-356(1999)).
[2]
SEQUENCE FROM N.A. (ISOFORM 2), AND CHARACTERIZATION.
TISSUE=Brain;
MEDLINE=20408933; PubMed=10851242;
RA Elshourbagy N.A., Ames R.S., Fitzgerald L.R., Foley J.J.,
Chambers J.K., Szekeres P.G., Evans N.A., Schmidt D.B., Buckley P.T.,
Dytko G.M., Murdock P.R., Milligan G., Groarke D.A., Tan K.B.,
Shabon U., Nuthulaganti P., Wang D.Y., Wilson S., Bergsma D.J.,
Sarau H.M.;
RT "Receptor for the pain modulatory neuropeptides FF and AF is an orphan
G-protein-coupled receptor.";
J. Biol. Chem. 275:25965-25971(2000).
[3]
SEQUENCE FROM N.A. (ISOFORM 2), AND CHARACTERIZATION.
TISSUE=Spinal cord;
MEDLINE=20564301; PubMed=11024015;
RA Bonini J.A., Jones K.A., Adham N., Forray C., Artymyshyn R.,
Dukhin M.M., Smith K.B., Tamm J.A., Boteju L.W., Lakhiani P.P.,
Raddatz R., Yao W.-J., Ogozalek K.B., Boyle N., Kouranova E.V.,
Quan Y., Vayesse P.J., Wetzel J.M., Branchek T.A., Gerald C.,
Borowsky B.;
RT "Identification and characterization of two G protein-coupled
receptors for neuropeptide FF.";
J. Biol. Chem. 275:39324-39331(2000).
[4]
SEQUENCE FROM N.A. (ISOFORM 3).
MEDLINE=20299143; PubMed=10837915;
RA Parker R.M.C., Copeland N.G., Eyre H.J., Liu M., Gilbert D.J.,
Crawford J., Couzens M., Sutherland G.R., Jenkins N.A., Herzog H.;
RT "Molecular cloning and characterization of GPR74 a novel G-protein
coupled receptor closest related to the Y-receptor family.";
Brain Res. Mol. Brain Res. 77:199-208(2000).
[5]
SEQUENCE FROM N.A. (ISOFORM 2).
RA Liu Q., Guan X.-M., McDonald T.P., Jiang Q., Zeng Z., Marlene J.,
Williams D.L. Jr., Hong Y., Figueroa D., Clements M.K., Mallee J.,
Wang R., Evans J., Gould R., Austin C.P.;
RT "Identification and characterization of two cognate receptors for
mammalian EMRFamide-like neuropeptides.";
Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
[6]
SEQUENCE FROM N.A. (ISOFORM 4).
RA Laemmle B.S., Schindler M., Beilmann M., Hamilton B.S., Doods H.N.,
Wieland H.A.;
RT "Cloning and characterization of the NPGP receptor and identification
of a novel short mRNA isoform in human hypothalamus.";
Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
-!- FUNCTION: RECEPTOR FOR NPAF (A-18-P-AMIDE) AND NPPF (P-8-P-AMIDE)
ALSO BE ACTIVATED BY A VARIETY OF NATURALLY OCCURRING OR SYNTHETIC
FMRF-AMIDE LIKE LIGANDS. THIS RECEPTOR MEDIATES ITS ACTION BY
ASSOCIATION WITH G PROTEINS THAT ACTIVATE A PHOSPHATIDYLINOSITOL-
CALCIUM SECOND MESSENGER SYSTEM.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=4;
Comment=Experimental confirmation may be lacking for some
isoforms;
Name=1; Synonyms=long form;
IsoId=Q9YX53-1; Sequence=Displayed;
Name=2; Synonyms=short form;
IsoId=Q9YX53-2; Sequence=VSP_001907;
Name=3;
IsoId=Q9YX53-3; Sequence=VSP_001908, VSP_001909;
Name=4;
IsoId=Q9YX53-4; Sequence=VSP_001910, VSP_001911;
-!- TISSUE SPECIFICITY: Isoform 1 is abundant in placenta. Relatively
highly expressed in thymus, testis, and small intestine. Expressed
at low levels in several tissues including spleen, prostate,
brain, heart, ovary, colon, kidney, lung, pancreas and
not expressed in skeletal muscle and leukocytes. Highest but

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RA Kodukula K., Kienzie B., Seethala R.;
 RT "Cloning and functional expression of a cDNA encoding a human type 2
 RT neurotrophin Y receptor.";
 RT J. Biol. Chem. 270:22661-22664 (1995).
 RN [4].
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96209786; PubMed=8643460;
 RA Yan H., Yang J., Marasco J., Yamaguchi K., Brenner S., Collins F.,
 RA Karbon W.;
 RT "Cloning and functional expression of cDNAs encoding human and rat
 RT pancreatic polypeptide receptors.";
 RT Proc. Natl. Acad. Sci. U.S.A. 93:4661-4665 (1996).
 RL [5].
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97131518; PubMed=8975716;
 RA Ammar D.A., Eadie D.M., Wong D.J., Ma Y.-Y., Kolakowski L.F. Jr.,
 RA Yang-Peng T.L., Thompson D.A.;
 RT "Characterization of the human type 2 neurotrophin Y receptor gene
 RT (NPY2R) and localization to the chromosome 4q region containing the
 RT type 1 neurotrophin Y receptor gene.";
 RL Genomics 38:392-398 (1996).
 RP [6].
 RP SEQUENCE FROM N.A.
 RA Zastawny R.L.;
 RT "Human neurotrophin Y Y2 receptor gene.";
 RL Submitted (Oct-1996) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: RECEPTOR FOR NEUROPEPTIDE Y AND PEPTIDE YY. THE RANK
 CC ORDER OF AFFINITY OF THIS RECEPTOR FOR PANCREATIC POLYPEPTIDES IS
 CC PYY > NPY > PYY (3-36) > NPY (2-36) > [ILE-31, GLN-34] PP >
 CC [LEU-31, PRO-34] NPY > PP, [PRO-34] PYY AND NPY FREE ACID.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: HIGH LEVELS IN AMYGDALA, CORPUS CALLOSUM,
 CC HIPPOCAMPUS AND SUBTHALAMIC NUCLEUS. ALSO DETECTABLE IN CAUDATE
 CC NUCLEUS, HYPOTHALAMUS AND SUBSTANTIA NIGRA.
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC HIGHEST TO TACHYKININ RECEPTORS.
 CC
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 CC or send an email to license@isb-sib.ch.
 CC
 DR EMBL; U36269; AAC50281.1; -;
 DR EMBL; U42766; AAB04120.1; -;
 DR EMBL; U32500; AAB03170.1; -;
 DR EMBL; U42389; AAB07760.1; -;
 DR EMBL; U50146; AAC51115.1; -;
 DR EMBL; U76254; AAD00248.1; -;
 DR PIR; I39187; I39187.
 DR Genes; HGNC:7957; NPY2R.
 DR MIM; 162642; -;
 DR GO; GO:0005887; C: integral to plasma membrane; TAS.
 DR GO; GO:0005246; F: calcium channel regulator activity; TAS.
 DR GO; GO:0004983; F: neuropeptide Y receptor activity; TAS.
 DR GO; GO:0004872; F: receptor activity; TAS.
 DR GO; GO:0007193; P: G-protein signaling, adenylate cyclase inhib.; TAS.
 DR GO; GO:0007626; P: locomotory behavior; TAS.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm1.1.
 DR PRINTS; PR00237; GPCR_Rhodopsn.
 DR PROSITE; PS00237; G-PROTEIN RECEPTOR F1.1; 1.
 DR PROSITE; PS0262; G-PROTEIN RECEPTOR F1.2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Phosphorylation; Lipoprotein; Palmitate
 FT DOMAIN 1 49 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 50 72 1 (POTENTIAL).
 FT DOMAIN 73 82 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 83 104 2 (POTENTIAL).
 FT DOMAIN 105 124 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 125 146 3 (POTENTIAL).

FT DOMAIN 147 166 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 167 187 4 (POTENTIAL).
 FT DOMAIN 188 214 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 215 240 5 (POTENTIAL).
 FT DOMAIN 241 268 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 269 291 6 (POTENTIAL).
 FT DOMAIN 292 304 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 305 328 7 (POTENTIAL).
 FT DOMAIN 329 381 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 11 11 N-LINKED (GLCNAC...) (POTENTIAL).
 FT DISULFID 123 203 BY SIMILARITY.
 FT LIPID 342 342 PALMITATE (POTENTIAL).
 FT CONFLICT 134 134 V -> A (IN REF. 3).
 FT CONFLICT 172 172 A -> G (IN REF. 4).
 FT CONFLICT 174 174 G -> R (IN REF. 4).
 FT CONFLICT 202 202 A -> P (IN REF. 4).
 FT CONFLICT 209 209 G -> A (IN REF. 4).
 FT CONFLICT 248 248 N -> S (IN REF. 6).
 FT CONFLICT 311 311 H -> Y (IN REF. 6).
 SQ SEQUENCE 381 AA; 42731 MW; 7D018C0169597BC7 CRC64;
 Query Match 21.0%; Score 469.5; DB 1; Length 381;
 Best Local Similarity 31.0%; Pred. No. 3.5e-26;
 Matches 113; Conservative 75; Mismatches 123; Indels 53; Gaps 13;
 QY 38 BELPGRKMI-----ALVLTGVLFALALFGNALVYVYVTRSKAMRTVTNIFICSLALS 92
 DB 38 PELDSIKLAEVQVVLVLAICSIILLGVNLSLVHVIKFSMTVTNFIANLAVADL 97
 QY 93 LITFPCIPVTMLQNIISNWLGGAFICKGVFPVQSTAVVTILMTCTIAVERHQGLVHPFK 152
 DB 98 LVNTLCIPFTLTYYTLMGEMKGPVLCHLPVQAQGLAVQVSTITLTVALDRHRCIVVHLE 157
 QY 153 MKQVYTRERATMLGVVNLVAVIVGSPMWHVQV---LEIKYVDLYEKEHICCLPEW---T 206
 DB 158 SK-ISKREISLIIIGLAWGSALLASPLAFREVSLEIIPDF-----EIVACTEKWPGE 211
 QY 207 SPVHQKIYTTTFLVILPLMLVLLIYSGIYELW--IKRVDGDSVLRTIHKEMSKI 264
 DB 212 KSIYGVTVSLSLIIVLPGLIISFSYTRI---WSKLNHVSPGAANDHYH----- 260
 QY 265 ARKKRAVIMVMTVVALPANCWAFHVHVMIEYSNFE---KEYDDVTIKMIPAIVQIIG 321
 DB 261 -ORRQCKTLMVLCVWVFAVSWLPHAPQLAVDIDSQVLDLKEY-----KLIFTFPHIA 314
 QY 322 PENSICNPVYAFNMENFNKNVLSAVCYCVNKTFSPAQR-----HGNSGITMREKAKFS 377
 DB 315 MCSTFANPLLYGMNNSYRKAFLSA-----FRCEQLDAIHSEVSVTFKAK-NLE 364
 QY 378 LREN 381
 DB 365 VRKN 368
 RESULT 4
 NY2R_MACMU STANDARD; PRT; 381 AA.
 AC Q9GK74;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Neuropeptide Y receptor type 2 (NPY2-R) (NPY-Y2 receptor).
 GN NPY2R.
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Macaca.
 OX NCBI_TaxID=9544;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21184974; PubMed=11287088;
 RA Gehlert D.R., Yang P., George C., Wang Y., Schober D.,
 RA Gackenhimer S., Johnson D., Beavers L.S., Gadske R.A., Baez M.;


```

RT Cloning and characterization of Rhesus monkey neuropeptide Y receptor
RL Peptides 22:343-350 (2001).
CC -|- FUNCTION: RECEPTOR FOR NEUROPEPTIDE Y AND PEPTIDE YY.
CC -|- SUBCELLULAR LOCATION: Integral membrane protein.
CC -|- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC HIGHEST TO TACHYKININS RECEPTORS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF303090; AAG40772.1; -.
CC InterPro; IPR000276; GPCR_Rhodpsn.
CC Pfam; PF00001; 7tm1; 1.
CC PRINTS; PR00237; GPCRHOPOPSN.
CC PROSITE; PS00237; G-PROTEIN RECEPTOR FL1; 1.
CC PROSITE; PS0262; G-PROTEIN RECEPTOR FL2; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein;
CC Phosphorylation; Lipoprotein; Palmitate.
CC DOMAIN 1 49 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 50 72 1 (POTENTIAL).
CC DOMAIN 73 82 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 83 104 2 (POTENTIAL).
CC DOMAIN 105 124 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 125 146 3 (POTENTIAL).
CC DOMAIN 147 166 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 167 187 4 (POTENTIAL).
CC DOMAIN 188 214 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 215 240 5 (POTENTIAL).
CC DOMAIN 241 268 6 (POTENTIAL).
CC TRANSMEM 269 291 7 (POTENTIAL).
CC DOMAIN 292 304 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 305 328 7 (POTENTIAL).
CC DOMAIN 329 381 CYTOPLASMIC (POTENTIAL).
CC CARBOHYD 11 11 N-LINKED (GLCNAC. .) (POTENTIAL).
CC DISULFID 123 203 BY SIMILARITY.
CC LIPID 342 342 PALMITATE (POTENTIAL).
CC SEQUENCE 381 AA; 42729 MW; D589D691DC05A49D CRC64;
Query Match 21.0%; Score 468.5; DB 1; Length 381;
Best Local Similarity 30.8%; Pred. No. 4.1e-26;
Matches 112; Conservative 76; Mismatches 123; Indels 53; Gaps 13;
QY 38 PELPGRKLV-----ALVLTGLVLIIPALFGNALFYVYVTRSKAMRTVNTIFICLSLSD 92
DB 38 PELIDTKLIEVQVVLILAYCSIIILGVIGNSLVHVIKPKSMRTVTNFFIANLAV 97
QY 93 LITFFCIPVIMLQNISDNWLGGAFCIKWVPFQSTAVVTEILTMTCIAVERHQGLVHPFK 152
DB 98 VVNTLCPLFTLYTLMGWEKMGVPLCHLVPAQGLAVQVSTITVIALDRHRCIVHLE 157
QY 153 MKQVYTNRAFTMLGVVWLVAIVGSPMHWVQ---LEIKYDFLYEKEHICCLSEW--T 206
DB 158 SK--ISKRIISFLITGLAWGISALLASPLAIFREYSLIEIIPDF---EIVACTEKWPCEE 211
QY 207 SPVHQKYTYTIFILVILFLPLMWMILLYSKIGYELW--IKKRVGDGSLVRIHKGKMSKI 264
DB 212 KSIYGVTVYSSLLILVLPGLGISYFSYTRI---WSKLSHVSPPGANDHYH----- 260
QY 265 ARKKRAVIMMVTIVVAVFVAVCWAPFHVHVMHIEYNFE---KEYDDVTIKMFAIVQIIG 321
DB 261 -QRQKTKMLVCVVVFAVSNLPLHAFQALDAVIDSHVLDLKEY-----KLITVFVHIA 314
QY 322 FNSNIGNPVIVAFNNEPKNVLSAVCYIVNKTFSPAQR-----HGNSGITMWRKAKPS 377
DB 315 MCSTFANPLLYGWNNSVYKRAFLSA-----FRCEQRDLAIHSEVSTFRKAK-NLE 364
QY 378 LREN 381

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Db 365 VRKN 368
:|:|

RESULT 5

NY2R_PIG

ID NY2R_PIG STANDARD; PRT; 382 AA.

AC O02836; Q9TS11;

DT 15-JUL-1998 (Rel. 36, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Neuropeptide Y receptor type 2 (NPY2-R) (NPY-Y2 receptor).

GN NPY2R.

OS Sus scrofa (Pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

OX NCBI_TaxID=9823;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Spleen;

RX MEDLINE=99017380; PubMed=9802394;

RA Malmstrom R.E., Hoekfelt T., Bjoerkman J.-A., Nihlen C., Bystrom M.,

RA Ekstrand A.J., Lundberg J.M.;

RT "Characterization and molecular cloning of vascular neuropeptide Y

receptor subtypes in pig and dog.";

RL Regul. Pept. 75:55-70(1998).

RN [2]

RP REVISION TO 207.

RA Ekstrand A.J.;

RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RA Wraith A., Tornsten A., Chardon P., Harbitz I., Chowdhary B.P.,

RA Andersson L., Larhammar D.;

RT "Porcine NPY receptors NPY1R, NPY2R and NPY5R: cloning, mapping and

comparative analysis.";

RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.

CC -|- FUNCTION: RECEPTOR FOR NEUROPEPTIDE Y AND PEPTIDE YY.

CC -|- SUBCELLULAR LOCATION: Integral membrane protein.

CC -|- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

CC HIGHEST TO TACHYKININS RECEPTORS.

CC -----

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CC -----

CC EMBL; AF005780; AAC26670.2; -.

CC EMBL; AF106082; AAD13777.1; ALT_INIT.

CC HSP; P02699; 1F88.

CC InterPro; IPR000276; GPCR_Rhodpsn.

CC Pfam; PF00001; 7tm1; 1.

CC PRINTS; PR00237; GPCRHOPOPSN.

CC PROSITE; PS00237; G-PROTEIN RECEPTOR FL1; 1.

CC PROSITE; PS0262; G-PROTEIN RECEPTOR FL2; 1.

CC G-protein coupled receptor; Transmembrane; Glycoprotein;

Phosphorylation; Lipoprotein; Palmitate.

FT DOMAIN 1 50 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 51 73 1 (POTENTIAL).

FT DOMAIN 74 83 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 84 105 2 (POTENTIAL).

FT DOMAIN 106 125 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 126 147 3 (POTENTIAL).

FT DOMAIN 148 167 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 168 188 4 (POTENTIAL).

FT DOMAIN 189 215 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 216 241 5 (POTENTIAL).

FT DOMAIN 242 269 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 270 292 6 (POTENTIAL).

FT DOMAIN 293 305 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 306 329 7 (POTENTIAL).

FT DOMAIN 330 382 CYTOPLASMIC (POTENTIAL).

FT CARBOHYD 11 11 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT DISULFID 124 204 BY SIMILARITY.

FT LIPID 343 343 PALMITATE (POTENTIAL).

FT CONFLICT 4 4 I -> L (IN REF. 3).

FT CONFLICT 179 179 L -> V (IN REF. 3).

FT CONFLICT 215 215 I -> N (IN REF. 3).

FT CONFLICT 366 366 A -> V (IN REF. 3).

SQ SEQUENCE 382 AA; 42556 MW; 5C01FAF3A0423858 CRC64;

Query Match 20.9%; Score 467.5; DB 1; Length 382;

Best Local Similarity 30.7%; Pred. No. 4.9e-26;

Matches 119; Conservative 75; Mismatches 128; Indels 65; Gaps 14;

QY 38 PELPGRAKL-----ALVLTGVLPALFALFONALFVYVTRSKAMRTVTNIFICSLALS 92

Db 39 PELKDSKLEIVQVILILAYCSILLGVVGNLSIVHVIKFSKMTVTNFFIANLAVADL 98

QY 93 LITFFCIPVMTLQNI SDNLGGAFCIKWPFVOSTAVVTEILMTCTIAVERHOGLVHPFK 152

Db 99 LVNTLCPLPFTLTTLGMEKWKGPVLCVLAQGLAVQVSTITLTVIALDRHRCIVVHLE 158

QY 153 MKQYTNRRAPFTMLGVVWLVAIVGSPMHVQV---LEIKYDFLYEKEHICCLEEW---T 206

Db 159 SK--ISKRISFLIIGLAWGISALLASPLAFREYSLEIIPDF----EIVACTEKWPGEE 212

QY 207 SPVHQKIYTFILVILFLPLMWMILYKIGYELW---IKRVGDSGLVLRTHGKEMSKI 264

Db 213 KSIYGTIVYSSLLILVLPGLGISFYARI----WSKLNHVSPPGVNDHYH----- 261

QY 265 ARKKRAVIMMVTVALFVAVCWAPFHVHMMIEYSNFE---KEYDDVTIKMIFAIQIIG 321

Db 262 -QRQKTKMLVGVVVFVAVSWPLHAPQLAVDIDSVQLDKEY-----KLIFTVPHIIA 315

QY 322 FNSNICHPIVAFNENPKXNVLSAVCYCVNKTFSPAQR----HGNSGITMMKREKAPS 377

Db 316 MCSTFANPLLYGMWNSYRKAFLSA-----FRCEQRDAIHSEVSMT---SKAKN 363

QY 378 LRENPEETKGEAFSDGNIEVKCEQT 404

Db 364 L-----EATKNGPDDSFTEAT 380

RESULT 6

NY2R_BOVIN STANDARD; PRT; 384 AA.

AC P9113;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE Neuropeptide Y receptor type 2 (NPY2-R) (NPY-Y2 receptor).

GN NPY2R.

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

OC Bovidae; Bovinae; Bos.

OX NCBI_TaxID=9913;

RN [1]

RP SEQUENCE FROM N.A.

RA Annar D.A., Kolakowski L.F. Jr., Eadie D.M., Wong D.J., Ma Y.Y.,

RA Yang-Peng T.L., Thompson D.A.

RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.

CC -!- FUNCTION: RECEPTOR FOR NEUROPEPTIDE Y AND PEPTIDE YY.

CC -!- SUBCELLULAR LOCATION: Integral membrane protein.

CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

CC HIGHEST TO TACHYKININS RECEPTORS.

CC -----

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CC -----

DR EMBL; U50144; AAB40600.1; -

DR InterPro; IPR000276; GPCR_Rhodopsin.

DR Pfam; PF00001; 7tm_1; 1.

DR PRINTS; PR00237; GPCRHHODOPS.

DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL1; 1.

DR PROSITE; PS00262; G-PROTEIN RECEPTOR FL2; 1.

DR G-protein coupled receptor; Transmembrane; Glycoprotein;

KW Phosphorylation; Lipoprotein; Palmitate.

FT DOMAIN 1 52 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 53 75 1 (POTENTIAL).

FT DOMAIN 76 85 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 86 107 2 (POTENTIAL).

FT DOMAIN 108 127 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 128 149 3 (POTENTIAL).

FT DOMAIN 150 169 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 170 190 4 (POTENTIAL).

FT DOMAIN 191 217 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 218 243 5 (POTENTIAL).

FT DOMAIN 244 271 6 (POTENTIAL).

FT TRANSMEM 272 294 7 (POTENTIAL).

FT DOMAIN 295 307 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 308 331 7 (POTENTIAL).

FT DOMAIN 332 384 CYTOPLASMIC (POTENTIAL).

FT CARBOHYD 13 13 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT DISULFID 126 206 BY SIMILARITY.

FT LIPID 345 345 PALMITATE (POTENTIAL).

SQ SEQUENCE 384 AA; 42943 MW; 468D19CBA8F29681 CRC64;

Query Match 20.9%; Score 467; DB 1; Length 384;

Best Local Similarity 31.5%; Pred. No. 5.3e-26;

Matches 112; Conservative 72; Mismatches 120; Indels 52; Gaps 12;

QY 38 PELPGRAKL-----ALVLTGVLPALFALFONALFVYVTRSKAMRTVTNIFICSLALS 92

Db 41 PELDSTKLEIVQVILILAYCSILLGVVGNLSIVHVIKFSKMTVTNFFIANLAVADL 100

QY 93 LITFFCIPVMTLQNI SDNLGGAFCIKWPFVOSTAVVTEILMTCTIAVERHOGLVHPFK 152

Db 101 LVNTLCPLPFTLTTLGMEKWKGPVLCVLAQGLAVQVSTITLTVIALDRHRCIVVHLE 160

QY 153 MKQYTNRRAPFTMLGVVWLVAIVGSPMHVQV---LEIKYDFLYEKEHICCLEEWSP- 208

Db 161 SK--ISKQISFLIIGLAWGISALLASPLAFREYSLEIIPDF----EIVACTEKWPGEE 214

QY 209 -VHQKIYTFILVILFLPLMWMILYKIGYELW---IKRVGDSGLVLRTHGKEMSKI 264

Db 215 KGIYGTIVYSSLLILVLPGLGISFYTRI----WSKLNHVSPPGAHHDYH----- 263

QY 265 ARKKRAVIMMVTVALFVAVCWAPFHVHMMIEYSNFE---KEYDDVTIKMIFAIQIIG 321

Db 264 -QRQKTKMLVGVVVFVAVSWPLHAPQLAVDIDSHVLDKEY-----KLIFTVPHIIA 317

QY 322 FNSNICHPIVAFNENPKXNVLSAVCYCVNKTFSPAQR----HGNSGITMMKREK 373

Db 318 MCSTFANPLLYGMWNSYRKAFLSA-----FRCEQRDAIHSEVSMTFKAKK 364

RESULT 7

NY2R_MOUSE STANDARD; PRT; 385 AA.

AC P97295;

DT 15-JUL-1998 (Rel. 36, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE Neuropeptide Y receptor type 2 (NPY2-R) (NPY-Y2 receptor).

GN NPY2R.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;


```

CC      or send an email to license@sib-sib.ch).
CC      -----
CC      EMBL; AF041246; AAC40042.1; -.
CC      InterPro; IPR000276; GPCR_Rhodpsn.
CC      InterPro; IPR004060; Orexin_receptor2.
CC      Pfam; PF00001; 7tm_1; 1.
CC      Pfam; PF03827; Orexin_rec2; 1.
CC      PRINTS; PRO0237; GPCRHHODPSN.
CC      PRINTS; PRO1522; OREXIN2R.
CC      PROSITE; PS00237; G-PROTEIN RECP_F1_1; 1.
CC      PROSITE; PS0262; G-PROTEIN RECP_F1_2; 1.
CC      G-protein coupled receptor; Transmembrane; Glycoprotein.
CC      DOMAIN 1 54 EXTRACELLULAR (POTENTIAL).
CC      TRANSSEM 55 75
CC      DOMAIN 76 88
CC      TRANSSEM 89 110
CC      DOMAIN 111 127
CC      TRANSSEM 128 150
CC      DOMAIN 151 172
CC      TRANSSEM 173 193
CC      DOMAIN 194 224
CC      TRANSSEM 225 247
CC      DOMAIN 248 304
CC      TRANSSEM 305 327
CC      DOMAIN 328 342
CC      TRANSSEM 343 366
CC      DOMAIN 367 460
CC      CARBOHYD 14 14
CC      TRANSSEM 22 22
CC      CARBOHYD 202 202
CC      N-LINKED (GLCNAC. .) (POTENTIAL).
CC      N-LINKED (GLCNAC. .) (POTENTIAL).
CC      SEQUENCE 460 AA; 52489 MW; 3844E3D8F8B85D5 CRC64;

Query Match      20.6%; Score 459.5; DB 1; Length 460;
Best Local Similarity 26.0%; Pred. No. 2.1e-25;
Matches 118; Conservative 97; Mismatches 164; Indels 75; Gaps 11;

QY      4 LNITPEPSRLRLDHLNLTREOFIALYRLPLVYTPTELPGRAKLALVTGLVLFALALPGN 63
DB      21 LNITQEPF---LNPTDXDDEEFLR-YLWREYLH---PKYEWVLVLAGYIIVFVVALIGN 72
QY      64 ALVYVYVTRSKAMTVTNIFCSLALSDLLATFFCIPVTMLQNSDNLWLGAFCKVVPF 123
DB      73 VLVCVAVKNNHMTVNTVNFVNLADLVLTITCLPATLVVDITETWFFQOSLCKVIPY 132
QY      124 VQSTAVTEILTMTCIAVERHQGLVHPKMKWQVTRRAFTMLGVLVAVIVGSPMWHV 183
DB      133 LQTVSVSVSLTSCIALDRVVAICHPLMFK--STAKPARNISVIVVIVSCIIIMPOAIV 190
QY      184 QOLEIKYDFLYEKHEI--CCLEEWTSVHQKIYTTFFILVILFLPLMVMMLYLSKIGYEL 241
DB      191 MERSSMLPLGLANKTTLTFTVCDERWGEVYPKWYHICFPLVTYMAPCLMLVLAQLIFRKL 250
QY      242 WIKKRVGDSGLR-----TIHGKEMSKIARKKRAVIMVTV 278
DB      251 WCRIPGTSSVQKRWQKQPQVPSRGGQOSKARISAAVAEIKQIRARRRTAKMLAV-V 309
QY      279 VALFVACWAPHHVHMMEI-YSNFEKEYDDVTIKMFAIVQIIGFSNCSNPIVAFMNE 337
DB      310 LLVFAICVLPISILNLKRVKVEGFTHTEDRETVAWFTTSHWLVYANSAANPIIYNFLSG 369
QY      338 NFKKNVLISAVCYICVNTFTSPAQRHGNSGITMKRKKAKFSLRENPVETKGEAFSDGNI 397
DB      370 KFREEFKAAAFSCCL-----GVHRRQDRLARGR-- 397
QY      398 VKLCEQTEKKKLKRHLALFR--SELAENSPDS 429
DB      398 ----TSTESKSLTQISFNPNVSKLSEHALTS 427

RESULT 10
NY2R CAVPO
ID_NY2R CAVPO
AC Q922D5;

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DT      30-MAY-2000 (Rel. 39, Created)
DT      30-MAY-2000 (Rel. 39, Last sequence update)
DT      30-MAY-2000 (Rel. 39, Last annotation update)
DE      Neuropeptide Y receptor type 2 (NPY2-R) (NPY-Y2 receptor).
GN      NPY2R.
OS      Cavia porcellus (Guinea pig).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX      NCBI_TaxID=10141;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      MEDLINE=99017376; PubMed=9802390;
RA      Sharma P.S., Holmberg S.K., Eriksson H., Beck-Sickinger A.G.,
RA      Grundemar L., Larhammar D.;
RA      "Cloning and functional expression of the guinea pig neuropeptide Y
RT      Y2 receptor.";
RL      Regul. Pept. 75:23-28(1998).
CC      -!- FUNCTION: RECEPTOR FOR NEUROPEPTIDE Y AND PEPTIDE YY.
CC      -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC      -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC      HIGHEST TO TACHYKININS RECEPTORS.
CC      -----
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CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@sib-sib.ch).
CC      -----
CC      EMBL; AF072821; AAD13143.1; -.
CC      InterPro; IPR000276; GPCR_Rhodpsn.
CC      Pfam; PF00001; 7tm_1; 1.
CC      PRINTS; PRO0237; GPCRHHODPSN.
CC      PROSITE; PS00237; G-PROTEIN RECP_F1_1; 1.
CC      PROSITE; PS0262; G-PROTEIN RECP_F1_2; 1.
CC      G-protein coupled receptor; Transmembrane; Glycoprotein;
CC      Phosphorylation; Lipoprotein; Palmitate.
CC      DOMAIN 1 50 EXTRACELLULAR (POTENTIAL).
CC      TRANSSEM 51 73
CC      DOMAIN 74 83
CC      TRANSSEM 84 105
CC      DOMAIN 106 125
CC      TRANSSEM 126 147
CC      DOMAIN 148 167
CC      TRANSSEM 168 188
CC      DOMAIN 189 215
CC      TRANSSEM 216 241
CC      DOMAIN 242 269
CC      TRANSSEM 270 292
CC      DOMAIN 293 305
CC      TRANSSEM 306 329
CC      DOMAIN 330 381
CC      CARBOHYD 11 11
CC      DISULFID 124 204
CC      LIPID 343 343
CC      PALMITATE (POTENTIAL).
CC      SEQUENCE 381 AA; 42342 MW; D806B859A43EAC CRC64;

Query Match      20.4%; Score 457; DB 1; Length 381;
Best Local Similarity 30.3%; Pred. No. 2.7e-25;
Matches 108; Conservative 75; Mismatches 123; Indels 50; Gaps 12;

QY      38 PELPGRAKL-----ALVLTGLVLFALALPGNALVFVVTFSKAMRVTNIFCSLALSDL 92
DB      39 PELIDSTKTEVRVLIILAYCSIIILGVGNSLVHVIKFSKMTVTNFFIANLAVADL 98
QY      93 LIITFCIPVTMLQNSDNLWLGAFICKMVPFVQSTAVVTBIITMTCTIAVERHQGLVHPFK 152
DB      99 LVNLTCLPLFTLYTLMGEKWKGVFLCHVPAQGLAVQVSTVTLTVALDRHRCIVHLD 158
QY      153 MKVQYTRRAFTMLGVVVLVAVIVGSPMMHVQ---LEIKYDFLYEKHEICILEW---T 206
DB      159 SK--ISKQNSFLIIGLAWGISALLASFLAIFREYSLEIIPDF---EIVACTEKVPGE 212

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QY 207 SPVHQKIYTTFLVLFLPLMVLMLILYSKIGVLM--IKRVGDGSLVLTIRHGKMSKI 264
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 213 KSIYGTWYLSLILVLPLGLGISVYVRI-----WSKLNHYSPGAANDHYH----- 261
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 265 ARKKKAVINMVTVALFAVCWAPPHVHMVMEYSNFE---KEYDDVTIKMFAIVQIIG 321
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 262 -QRQKTKMLVFWVVVFAVWMLPLHAFQLAVDIDSQVLDLKEY-----KLIFTVEHIIA 315
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 322 FNSNICNPIVAFNMENFKKNVLISAV-C-----YCVNKTSPQAORHGNSG 366
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 316 MCSTFANPLLYGMNSNYRKAFLSARFCQORLDAIQSEVCTVKAKINWEVEKNHG 371
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 11
ID -OX2R_HUMAN STANDARD; PRT; 444 AA.
AC O43674;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE Orexin receptor type 2 (Ox2r) (Hypocretin receptor type 2).
GN HCRT2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98150861; PubMed=9491897;
RA Sakurai T., Amemiya A., Ishii M., Matsuzaki I., Chenelli R.M.,
RA Tanaka H., Williams S.C., Richardson J.A., Kozlowski G.P., Wilson S.,
RA Arch J.R.S., Buckingham R.E., Haynes A.C., Carr S.A., Annan R.S.,
RA McNulty D.E., Liu W.-S., Terrett J.A., Elshourbagy N.A., Bergsma D.J.,
RA Yanagisawa M.;
RT "Orexins and orexin receptors: a family of hypothalamic neuropeptides
RT and G protein-coupled receptors that regulate feeding behavior.";
RL Cell 92:573-585(1998).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21580342; PubMed=11723285;
RA Olafsdottir B.R., Rye D.B., Scammell T.E., Matheson J.K.,
RA Stefansson K., Gulcher J.R.;
RT "polymorphisms in hypocretin/orexin pathway genes and narcolepsy.";
RL Neurology 57:1896-1899(2001).
RN [3]
RP REVIEW.
RX MEDLINE=21237974; PubMed=11340621;
RA Hungs M., Mignot E.;
RT "Hypocretin/orexin, sleep and narcolepsy.";
RL Bioessays 23:397-408(2001).
RN [4]
RP REVIEW.
RX MEDLINE=21178476; PubMed=11283317;
RA Willie J.T., Chemelli R.M., Sinton C.M., Yanagisawa M.;
RT "To eat or to sleep? Orexin in the regulation of feeding and
RT wakefulness.";
RL Annu. Rev. Neurosci. 24:429-458(2001).
CC -!- FUNCTION: NONSELECTIVE, HIGH-AFFINITY RECEPTOR FOR BOTH OREXIN-A
CC AND OREXIN-B NEUROPEPTIDES.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DB EMBL; AF041245; AAC39602.1; -
DB EMBL; AY062031; AAL47215.1; -

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DR Genew; HGNC:4849; HCRT2.
DR MIM; 602393; -
DR GO; GO:0005887; C:integral to plasma membrane; TAS.
DR GO; GO:0008188; F:neuropeptide receptor activity; TAS.
DR GO; GO:0007631; P:feeding behavior; TAS.
DR GO; GO:0007218; P:neuropeptide signaling pathway; TAS.
DR GO; GO:0007268; P:synaptic transmission; TAS.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR InterPro; IPR004060; Orexin_receptor2.
DR Pfam; PF00001; 7tm_1; 1.
DR Pfam; PF03827; Orexin_rec2; 1.
DR PRINTS; PRO0237; GPCR_RHODOPSIN.
DR PRINTS; PRO1522; OREXIN2R.
DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS00262; G-PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 54
FT TRANSMEM 55 75
FT DOMAIN 76 88
FT TRANSMEM 89 110
FT DOMAIN 111 127
FT TRANSMEM 128 150
FT DOMAIN 151 172
FT TRANSMEM 173 193
FT DOMAIN 194 224
FT TRANSMEM 225 247
FT DOMAIN 248 304
FT TRANSMEM 305 327
FT DOMAIN 328 342
FT TRANSMEM 343 366
FT DOMAIN 367 444
FT CARBOHYD 14 14
FT CARBOHYD 22 22
FT CARBOHYD 202 202
SQ SEQUENCE 444 AA; 50680 MW; CA0669F0D4224C65 CRC64;

Query Match 20.4%; Score 455; DB 1; Length 444;
Best Local Similarity 27.7%; Pred. No. 4.3e-25;
Matches 104; Conservative 91; Mismatches 142; Indels 38; Gaps 9;

QY 4 LNITPEQFSRLRDHNLTRTEQFIALYLRPLVYVTELPGRAKLALVLTGLVIFALALFQN 63
Db 21 LNTEQEPF---LNPTDYDDEFFLR-YLRWEYLH----PKEYEWVLVAGVIVFVVALIGN 72
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 64 ALVFVWVTRSKAMRTVTNIFICSLASLLATFFCIPVTMLQNSIDNWLGGAFICKMVPF 123
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 73 VLVCAVWKNHMRITVNFVNLADLVITICLPATLVVDITETWFFGOSLCKVIPY 132
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 124 VQSTAVVTEILTMTCIAVERHQGLVHPFKMKQVNNRAFTMLGVVWLVAIVGSPMHV 183
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 133 LQTVSVSVSVLTLSIALDRWYAICHPLMFK--STAKGARNSVIIVISCIIMIPQAI 190
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 184 QOLEIKYDFLYEKHH--CCLSEWTSVPHQKIYTTFLVLFLPLMVLMLILYSKIGVEL 241
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 191 MECSTVFPGLANKTTLFTVCDERWGGEIYPRXHYHCPFLVYTMAPLCIMVLAYLQIFPK 250
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 242 WIKRVGDSGLR-----TIHGKMSKIARKKKRAVIMMVT 278
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 251 WCRQIPGTSSVQKWKPLQVSPRGQPTKRMASAAAEIKQIRARRRTARRMLV-V 309
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 279 VALFVCAVWAPPHVHMVMEI-YSNFEKEYDDVTIKMFAIVQIIGFNSNICNPIVAFNME 337
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 310 LLVEAICVLPISILNVLKRVFGMFAHTEDRFTVAVWTFSSHVWVYVANSANPIYNFLSG 369
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 338 NFKQNVLSAV-CYCI 351
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 370 KPFEFKAAFSCCCL 384
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 12
OX2R_CANFA
ID OX2R_CANFA
AC Q9TUF7;

```

DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Orexin receptor type 2 (Ox2r) (Hypocretin receptor type 2).
 GN HCRTR2.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN (1)
 RP SEQUENCE FROM N.A. PubMed=10458611;
 RX MEDLINE=9338793; PubMed=10458611;
 RA Lin L., Faraco J., Li R., Kadotani H., Rogers W., Lin X., Qiu X.,
 RA de Jong P.J., Nishino S., Mignot E.;
 RA "The sleep disorder canine narcolepsy is caused by a mutation in the
 RT hypocretin receptor 2 gene.";
 RL Cell 98:365-376(1999).
 RN (2)
 RP REVIEW.
 RX MEDLINE=21237974; PubMed=11340621;
 RA Hungs M., Mignot E.;
 RA "Hypocretin/orexin, sleep and narcolepsy.";
 RL Bioessays 23:397-408(2001).
 RN (3)
 RP REVIEW.
 RX MEDLINE=21178476; PubMed=11283317;
 RA Wallie J.T., Chemelli R.M., Sinton C.M., Yanagisawa M.;
 RA "To eat or to sleep? Orexin in the regulation of feeding and
 RT wakefulness.";
 RL Annu. Rev. Neurosci. 24:429-458(2001).
 RN (4)
 RP VARIANT NARCOLEPSY LYS-54, AND MUTAGENESIS OF GLU-54.
 RX MEDLINE=21180003; PubMed=11282968;
 RA Hungs M., Fan J., Lin L., Lin X., Maki R.A., Mignot E.;
 RA "Identification and functional analysis of mutations in the hypocretin
 RT (orexin) genes of narcoleptic canines.";
 RL Genome Res. 11:531-539(2001).
 CC -1- FUNCTION: NONSELECTIVE, HIGH-AFFINITY RECEPTOR FOR BOTH OREXIN-A
 CC AND OREXIN-B NEUROPEPTIDES.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- DISEASE: Defects in HCRTR2 are a cause of an autosomal recessive
 CC form of narcolepsy, observed in Labrador, doberman and
 CC dachshunds. Narcolepsy is a neurological sleep disorder affecting
 CC animals and humans, characterized by excessive daytime sleepiness,
 CC sleep fragmentation, symptoms of abnormal rapid-eye-movement
 CC (REM) sleep, such as cataplexy, hypnagogic hallucinations, and
 CC triggered paralysis. Cataplexy is a sudden loss of muscle tone
 CC triggered by emotions which is the most valuable clinical feature
 CC used to diagnose narcolepsy. As in humans, most cases of canine
 CC narcolepsy are sporadic but an autosomal recessive form was also
 CC observed.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC -----
 CC ENBL; AF164626; AAB49333.1; -
 DR InterPro; IPR000276; GPCR_Rhodopsin.
 DR InterPro; IPR004060; Orexin_receptor2.
 DR Pfam; PF00001; 7tm.1; 1.
 DR Pfam; PF03827; Orexin_rec2.1.
 DR PRINTS; PR00237; GPCR_Rhodopsin.
 DR PRINTS; PR01522; OREXIN2R.
 DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
 DR PROSITE; PS00262; G_PROTEIN_RECP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Disease mutation.
 FT DOMAIN 1 54 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 55 75 1 (POTENTIAL).
 FT DOMAIN 76 88 CYTOPLASMIC (POTENTIAL).
 FT TRANSEM 89 110 2 (POTENTIAL).
 FT DOMAIN 111 127 EXTRACELLULAR (POTENTIAL).
 FT TRANSEM 128 150 3 (POTENTIAL).
 FT DOMAIN 151 172 CYTOPLASMIC (POTENTIAL).
 FT TRANSEM 173 193 4 (POTENTIAL).
 FT DOMAIN 194 224 EXTRACELLULAR (POTENTIAL).
 FT TRANSEM 225 247 5 (POTENTIAL).
 FT DOMAIN 248 304 CYTOPLASMIC (POTENTIAL).
 FT TRANSEM 305 327 6 (POTENTIAL).
 FT DOMAIN 328 342 EXTRACELLULAR (POTENTIAL).
 FT TRANSEM 343 366 7 (POTENTIAL).
 FT DOMAIN 367 444 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 14 14 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 22 22 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 202 202 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARIANT 54 54 E -> K (IN AUTOSOMAL RECESSIVE
 FT NARCOLEPSY).
 FT MUTAGEN 54 54 E -> K: LOSS OF FUNCTION.
 SQ SEQUENCE 444 AA; 50675 MW; D848A4536D485D6B CRC64;
 Query Match 20.2%; Score 451; DB 1; Length 444;
 Best Local Similarity 27.7%; Pred. No. 8.2e-25;
 Matches 104; Conservative 90; Mismatches 143; Indels 38; Gaps 9;
 QY 4 LNITPQFSLRLDRHNLTRQFTALYELRLVYTPPLPGRAKLALVLTGLVLPALALFGN 63
 DB 21 LNITQEPF---LNPTDYDDDEFLR-VLWREYLH----PKSEYEWLIAGYIIVFVVALVGN 72
 QY 64 ALVFYVYVTRSKAMRTVTNIPICSLALSDDLITFCIPVTMLQNISDNWLGAPICKMVPF 123
 DB 73 VLVCVAVKNNHRTVTNYFIVNLSADLVLTITCLPATLVVDITETWTFGQSICKVIPY 132
 QY 124 VQSTAVTEILTMTCIAVERHQGLVHPFKMKQYTNRAFTMLGVVWLVAIVGVSPMHV 183
 DB 133 LQTVSVSVSLTSLCIALDRWAICHPLEK--STAKRANSIVIIWVSCIIMIPQAI 190
 QY 184 QQLLEIKYDELVEYKHEI--CCLEEWTSFVHOKIYTTTILVILFLLPLMVLILYSKIGYEL 241
 DB 191 MECSLMPLGLANKTTLFTVCDERWGGEIYPMKHICFFLVTYWAPLCMLVLAQLQIFRKL 250
 QY 242 WIKRRVGDGSLVR-----TIHGKEMSKIARKKKRAVIMMVTY 278
 DB 251 WCQIPICTSSVVRKMKPLQPAQSPRGQOTKSRISAVAAEIKQIRARKTARMMLV-V 309
 QY 279 VALPVCWAPFFVHVHMIE-YSNFEKEYDDVTIKMIPAIIVQIIGFSNISCNPVIYAFMNE 337
 DB 310 LLVFAICYLFIISILNVLKRVFGMFTHTEDRETVYAWFTFSGHVLVYANSAANPIYNFLSG 369
 QY 338 NPKKNVLSAV-CYCI 351
 DB 370 KFREEFKAAFSCCCL 384
 RESULT 13
 NY4R_MOUSE STANDARD; PRT; 375 AA.
 AC Q61041;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DE 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Neuropeptide Y receptor type 4 (NPY4-R) (Pancreatic polypeptide
 DE receptor 1) (Pr1) (NPYR-D).
 GN PPYR1 OR NPY4R.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=129/SV;
 RC MEDLINE=96193913; PubMed=8641440;

RA Gregor P., Millham M.L., Feng Y., Decarr L.B., McCaleb M.L.,
RA Cornfield L.J.;
RA "Cloning and characterization of a novel receptor to pancreatic
RT polypeptide, a member of the neurotensin Y receptor family.";
RL FEBS Lett. 381:58-62(1996).
CC -!- FUNCTION: RECEPTOR FOR NEUROPEPTIDE Y AND PEPTIDE YY. THE RANK
CC ORDER OF AFFINITY OF THIS RECEPTOR FOR PANCREATIC POLYPEPTIDES IS
CC PP >> PYY >= NPY.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: HEART, DETECTED IN SMALL INTESTINE.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC HIGHEST TO TACHYKININS RECEPTORS.
CC
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CC
CC EMBL; U40189; AAC52442.1; --
CC PIR; S63685; S63685.
CC MGI; MGI:105374; Ppy1.
CC GO; GO:0001602; Pancreatic polypeptide receptor activity; IDA.
CC GO; GO:0001601; Peptide YY receptor activity; IDA.
CC InterPro; IPR000276; GPCR_Rhodpsn.
CC Pfam; PF00001; 7tm 1; 1.
CC PRINTS; PR00237; GPCRHHODPSN.
CC PROSITE; PS00237; G-PROTEIN RECEPTOR F1_1; 1.
CC PROSITE; PS0262; G-PROTEIN RECEPTOR F2_1; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Phosphorylation; Lipoprotein; Palmitate.
FT DOMAIN 1 40 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 41 63 1 (POTENTIAL).
FT DOMAIN 64 74 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 75 95 2 (POTENTIAL).
FT DOMAIN 96 115 3 (POTENTIAL).
FT TRANSMEM 116 137 4 (POTENTIAL).
FT DOMAIN 138 157 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 158 178 5 (POTENTIAL).
FT DOMAIN 179 213 6 (POTENTIAL).
FT TRANSMEM 214 235 7 (POTENTIAL).
FT DOMAIN 236 288 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 289 301 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 302 325 7 (POTENTIAL).
FT TRANSMEM 326 375 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 2 2 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 19 19 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 29 29 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 187 187 N-LINKED (GLCNAC. .) (POTENTIAL).
FT DISULFID 114 201 BY SIMILARITY.
FT LIPID 340 340 PALMITATE (POTENTIAL).
SQ SEQUENCE 375 AA; 42634 MW; DFFD31775DBA310E CRC64;
Query Match 20.0%; Score 446.5; DB 1; Length 375;
Best Local Similarity 30.6%; Pred. No. 1.4e-24;
Matches 97; Conservative 72; Mismatches 121; Indels 27; Gaps 8;
QY 46 LALVLTGLVLI-FALALFGNALVFYVTRSKMRVTNIFICSLALSDLLITFFCIPVTML 104
DB 41 LAFITTVSIEITLGVGLNCLIFVTTRQKSNVTNLLIANLSDFLMCLICQPLVIT 100
QY 105 QNISDNWLGGAFCIKRWPFVQSTAVVTEITMTCTIAVERHQGLVHPFKMKQYTNKRAFT 164
DB 101 YTIMDYWIFGEVLCWMLTIQCMSTVLSLVVLEHQLIINP--TGMKPSIFQAVL 158
QY 165 MGVVWLVAVIVGSP-----MHWVQQLBKVDLYEKEHI CCLBEWTSFVHQKIYT 215
DB 159 GIWVWIFSCFLSLPFLANSTLNDLFFVNHKSV-VVEFLEDK--VVCVSWSSDHRRLIYT 215
QY 216 TFIILVFLPLMVMVILYLSKIGYELWIKKRVGDSGLVRLTHGKMSKIARKKRAVIMM 275

Db 216 TFLLLFOYCIPLAFILVCYIRIQLOFQKHV-----FHAACSSRAGOMKINSML 267
QY 276 VTVVALFVACWAPHVHVMMLEYENFKEYDDVVIKIMFPAIVQIGFNSNCINPIVYAPM 335
DB 268 MTWVTAFAVLPLPLHVFNTLEDW--YQSAIPACHGNLIFLMCHLLAMASTCVNPFYIGFL 325
QY 336 NENFKKNVLSAV--CYC 350
DB 326 NINFKDKIKALVLTCHC 342
RESULT 14
ID NY6R RABIT STANDARD; PRT; 371 AA.
AC P79217;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Neuropeptide Y receptor type 6 (NPY6-R).
GN NPY6R.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Japanese white; TISSUE=Skeletal muscle;
RX MEDLINE=97068888; PubMed=8910290;
RA Matsumoto M., Nomura T., Momose K., Ikeda Y., Kondou Y., Akiho H.,
RA Tosami J., Kimura Y., Okada M., Yamaguchi T.;
RT "Inactivation of a novel neuropeptide Y/peptide YY receptor gene in
RT primate species.";
RL J. Biol. Chem. 271:27217-27226(1996).
CC -!- FUNCTION: RECEPTOR FOR NEUROPEPTIDE Y AND PEPTIDE YY. THE ACTIVITY
CC OF THIS RECEPTOR IS MEDIATED BY G PROTEINS THAT INHIBITS ADENYLATE
CC CYCLASE ACTIVITY.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC HIGHEST TO TACHYKININS RECEPTORS.
CC
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CC
CC EMBL; D86521; BAA13104.1; --
CC InterPro; IPR000276; GPCR_Rhodpsn.
CC Pfam; PF00001; 7tm 1; 1.
CC PRINTS; PR00237; GPCRHHODPSN.
CC PROSITE; PS00237; G-PROTEIN RECEPTOR F1_1; 1.
CC PROSITE; PS0262; G-PROTEIN RECEPTOR F2_1; 1.
CC G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Phosphorylation; Lipoprotein; Palmitate.
FT DOMAIN 1 34 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 35 57 1 (POTENTIAL).
FT DOMAIN 58 69 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 70 90 2 (POTENTIAL).
FT DOMAIN 91 110 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 111 132 3 (POTENTIAL).
FT DOMAIN 133 152 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 153 174 4 (POTENTIAL).
FT DOMAIN 175 208 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 209 230 5 (POTENTIAL).
FT DOMAIN 231 261 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 262 284 6 (POTENTIAL).
FT DOMAIN 285 297 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 298 321 7 (POTENTIAL).
FT DOMAIN 322 371 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 11 N-LINKED (GLCNAC. .) (POTENTIAL).


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FT CARBOHYD 18 18 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 182 182 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 109 196 BY SIMILARITY.
FT LIPID 336 336 PALMITATE (POTENTIAL).
SQ SEQUENCE 371 AA: 42447 MW: 5847E358E320F24 CRC64;

Query Match 20.0%; Score 446; DB 1; Length 371;
Best Local Similarity 27.6%; Pred. No. 1.5e-24;
Matches 100; Conservative 93; Mismatches 117; Indels 52; Gaps 13;

QY 41 PGRALALVLGLVLFALALFQV-ALVFVVTNRKAMRTVTVNIFCSLALSDLLITFFCI 99
DB 31 PSLALLLLLIAYTVVLLGICGNSLSLTIIPKKQREARQVNTNILLANSLSDILVCVMCI 90
QY 100 PVTMLQNSDNWLGAFICKMPFFVQSTAVTEILTCTIAVERHOGVLVHPFKMKQVNTN 159
DB 91 PFTAIYTLMDRWIFQNTWCKTTSYQVSISVSIPLVLLAIERQLVNP--RGWKPSA 148
QY 160 RRAFTMLGVWMLAVIVGSPM---WHV-----QQLKIKYFLYEKEHICCLLEMTSPVHQ 211
DB 149 SHAYWGIMLIWFLSLLSIPLLSYHLTDEPRNLSPTD-LY-SHHVVVCEHWPFSKTQ 206
QY 212 KIYTFILAVILFLPLWMLILYKIGYELWIKKVGDSVLRTHGKMSKIARKK--- 268
DB 207 LLYSTSLIMQYFVPLGFMFICYLKI-----VICLH-KNSKIDRRRENE 250
QY 269 -----KRAVIMVMTVVALFAVCWAPFFVHMIEYSNFEKEDDVTK-----MFAIVQ 318
DB 251 SRLTENKINTMLISIVTFAACWPLNTFNVPDW-----YHEVLSCHHDLVFALCH 304
QY 319 IIGSNSICNPVIAFMNENFKKNVLSAVCYVKNKTSFPAQRHONGSI-TMRKXAKFS 377
DB 305 LVAMVSTCINLFLYFLNFKOLWLIHCL---CFALRERYENIAISTLHTDESXGS 361
QY 378 LR 379
DB 362 LR 363

RESULT 15
NY2R_CHICK
ID NY2R_CHICK STANDARD; PRT; 385 AA.
AC Q9DDN6;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Neuropeptide Y receptor type 2 (NPY2-R) (NPY-Y2 receptor).
GN NPY2R.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
CX NCBI_TaxID=9031;
EN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20532533; PubMed=11078884;
RA Salanek E., Holmberg S.K., Berglund M.M., Boswell T., Larhammar D.;
RT "Chicken neuropeptide Y receptor Y2: structural and pharmacological
RT differences to mammalian Y2";
RL FEBS Lett. 484:229-234(2000).
CC -!- FUNCTION: RECEPTOR FOR NEUROPEPTIDE Y AND PEPTIDE YY.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC HIGHEST TO TACHYKININS RECEPTORS.
CC -----
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CC -----
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DR EMBL; AF309091; AAG37898.1; -.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL 1; 1.
DR PROSITE; PS0262; G-PROTEIN RECEPTOR FL 2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Phosphorylation; Lipoprotein; Palmitate.
FT DOMAIN 1 53 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 54 76 1 (POTENTIAL).
FT DOMAIN 77 86 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 87 108 2 (POTENTIAL).
FT DOMAIN 109 128 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 129 150 3 (POTENTIAL).
FT DOMAIN 151 170 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 171 191 4 (POTENTIAL).
FT DOMAIN 192 218 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 219 244 5 (POTENTIAL).
FT DOMAIN 245 272 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 273 295 6 (POTENTIAL).
FT DOMAIN 296 308 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 309 332 7 (POTENTIAL).
FT DOMAIN 333 385 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 11 11 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT DISULFID 127 207 BY SIMILARITY.
FT LIPID 346 346 PALMITATE (POTENTIAL).
SQ SEQUENCE 385 AA; 43509 MW; 60A09B314E665B62 CRC64;

Query Match 19.7%; Score 440; DB 1; Length 385;
Best Local Similarity 25.5%; Pred. No. 4.2e-24;
Matches 119; Conservative 81; Mismatches 129; Indels 74; Gaps 16;

QY 23 BQRTALYRLPLVVT-----PELPGRAKALVLTGLVFA-----LALFGNAL 65
DB 19 ELFTKLYLDR---YTFVSELALDPKELKDSSTLVEVQI--ILLFVCSILLGVIGNSL 74
QY 66 VFYVTRSKAMRTVTNIFCSLALSDLLITFFCIPTVMTLQNSDNWLGAFICKMVPFVQ 125
DB 75 VIHVIKFSNRTVTNFFIANLAVADLLVNTLCPLFTLVTLGKWLGPVLCVLPVYQ 134
QY 126 STAVVTILTCTIAVERHOGVLVHPFKMKQVYTNRRAPTMGLGVVWLVAIVGSPMHWVQ 185
DB 135 ALAVHVSVTTLTIALDRHRCIVVHLESK--ISKRSIIGTIGVAVASALLASPLAIFRE 192
QY 186 --LEIKYDFLYEKEHICCLLEWTSPP---VHQKIYTTFFILVILFLPLWMLILYSKIGY 239
DB 193 YSLIEIIPDF---KIVVCEKWEQGLNGTIVSVSMLLIQVLPALIIISYATRI-- 246
QY 240 ELW--IKRVDGDSVLRTHGKMSKIARKKRAVIMMTVVALFVCAWAPFFVHMIE 297
DB 247 --WTKLNHVSPGAGNDHYH-----HRRQKTKMLVCVVVVFVSWLFFHAFQLVSD 296
QY 298 YSNFE---KEYDDVTIKMIFAIVQIIGFSNSICNPVIAFMNENFKKNVLSAVCYVKNK 354
DB 297 IDSQVLDLKEY-----KLIYTVFHVIAVCSCTFANPLLYGWMNNYRTAFITA----- 343
QY 355 TFSAPQRHGN-----SGITWRRKKAKSLRENVPVEETKGEAFS 392
DB 344 -FQCEQLDLSIHPEVSAFAFKARKKLEAKKSQFP-----GDSFT 380

Search completed: October 28, 2003, 10:10:36
Job time : 26 secs
```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 28, 2003, 10:08:35 ; Search time 100 Seconds
(without alignments)
1112.207 Million cell updates/sec

Title: US-10-070-241B-1

Perfect score: 2235

Sequence: 1 MQALNTPQFSRLRDHNL.....RHLALFRSELAENSPLDGSH 431

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: SPTEMBL 23.3

2: sp_archaea.*

3: sp_bacteria.*

4: sp_fungi.*

5: sp_human.*

6: sp_invertebrate.*

7: sp_mammal.*

8: sp_muc.*

9: sp_organelle.*

10: sp_phase.*

11: sp_plant.*

12: sp_rodent.*

13: sp_virus.*

14: sp_vertebrate.*

15: sp_unclassified.*

16: sp_rvitus.*

17: sp_bacteriap.*

18: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1972	88.2	455	4 Q96P65	Q96P65 homo sapien
2	1603	71.7	365	11 Q8BHH0	Q8BHH0 mus musculus
3	493.5	22.1	375	13 Q57463	Q57463 brachydanio
4	485	21.7	417	11 Q924H0	Q924H0 mus musculus
5	485	21.7	417	13 Q8BKR6	Q8BKR6 mus musculus
6	484.5	21.7	374	13 Q9YRX1	Q9YRX1 gadus morhu
7	479.5	21.5	377	13 Q73733	Q73733 brachydanio
8	479	21.4	381	11 Q9E3C0	Q9E3C0 rattus norv
9	475.5	21.3	405	11 Q924N0	Q924N0 mus musculus
10	468.5	21.0	377	13 Q8QGM3	Q8QGM3 gallus gall
11	466.5	20.9	381	11 Q8BWW1	Q8BWW1 mus musculus
12	460.5	20.6	460	11 Q8BGL2	Q8BGL2 mus musculus
13	452	20.2	373	13 Q73734	Q73734 brachydanio
14	450.5	20.2	375	11 Q8BZF9	Q8BZF9 mus musculus
15	433.5	19.4	449	5 Q9VB87	Q9VB87 drosophila
16	431	19.3	385	13 Q8QFM1	Q8QFM1 gallus gall

17	424	19.0	432	11	Q924G9	Q924G9 rattus norv
18	422.5	18.9	425	4	Q9HBV6	Q9HBV6 homo sapien
19	422	18.9	365	13	Q8UVM7	Q8UVM7 lampetia fl
20	421.5	18.9	364	11	Q8BV78	Q8BV78 mus musculus
21	421.5	18.9	383	6	Q9GK75	Q9GK75 macaca mula
22	417	18.7	402	5	Q964B5	Q964B5 dugesia tig
23	410	18.3	372	11	Q942D4	Q942D4 cavia porce
24	408.5	18.3	375	6	Q97505	Q97505 sus scrofa
25	408	18.3	429	5	P92045	P92045 lymnaea sta
26	405.5	18.1	422	11	Q8VHD7	Q8VHD7 rattus norv
27	404.5	18.1	431	5	Q8T8D1	Q8T8D1 urechis uni
28	404	18.1	517	5	Q8T0S8	Q8T0S8 drosophila
29	403.5	18.1	402	5	Q20275	Q20275 caenorhabdi
30	401	17.9	519	5	Q9VAD2	Q9VAD2 drosophila
31	400.5	17.9	504	5	Q9VGX8	Q9VGX8 drosophila
32	400.5	17.9	600	5	Q9VM75	Q9VM75 drosophila
33	398	17.8	457	5	Q18534	Q18534 caenorhabdi
34	394.5	17.7	481	5	Q9VNM1	Q9VNM1 drosophila
35	394.5	17.7	485	5	Q8SZ35	Q8SZ35 drosophila
36	390.5	17.5	517	5	Q9VWR3	Q9VWR3 drosophila
37	390.5	17.5	678	5	Q94736	Q94736 stomoxys ca
38	390	17.4	465	5	O44426	O44426 lymnaea sta
39	387.5	17.3	540	5	Q9VRM0	Q9VRM0 drosophila
40	385	17.2	411	13	Q9W6I3	Q9W6I3 gallus gall
41	384.5	17.2	370	13	Q8UWL5	Q8UWL5 fugu rubrip
42	379	17.0	397	5	Q9NHA4	Q9NHA4 boophilus m
43	377.5	16.9	423	5	Q964D4	Q964D4 periplaneta
44	376.5	16.8	598	5	Q9VMQ9	Q9VMQ9 drosophila
45	375.5	16.8	311	11	Q8R1R6	Q8R1R6 cavia porce

ALIGNMENTS

RESULT 1

Q96P65	ID	Q96P65	PRELIMINARY;	PRT;	455 AA.
AC	Q96P65;				
DT	01-DEC-2001 (TrEMBLrel. 19, Created)				
DT	01-DEC-2001 (TrEMBLrel. 19, Last sequence update)				
DT	01-MAR-2003 (TrEMBLrel. 23, Last annotation update)				
DE	G protein-coupled receptor.				
GN	GPR103.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=21458557; PubMed=11574155;				
RA	Lee D.K., Nguyen T., Lynch K.R., Cheng R., Vanti W.B., Arkhitko O.,				
RA	Lewis T., Evans J.F., George S.R., O'Dowd B.F.;				
RT	"Discovery and mapping of ten novel G protein-coupled receptor				
RT	genes.";				
RL	Gene 275:83-91(2001).				
DR	EMBL; AF411117; AAL26488.1;				
DR	InterPro; HGNC:15565; GPR103.				
DR	InterPro; IPR000883; COX1.				
DR	InterPro; IPR000276; GPCR_Rhodpsn.				
DR	Pfam; PF00001; 7tm 1; 1.				
DR	PRINTS; PF00115; COX1; 1.				
DR	PROSITE; PS00237; GPCRHOPOPSN.				
DR	PROSITE; PS00237; G PROTEIN RECEPT FL 1; 1.				
DR	PROSITE; PS00262; G-PROTEIN RECEPT FL 2; 1.				
DR	Receptor.				
SQ	SEQUENCE. 455 AA; 51742 MW; AA9B541CCFD36742 CRC64;				

Query Match 88.2%; Score 1972; DB 4; Length 455;
Best Local Similarity 89.8%; Pred. No. 8.9e-159;
Matches 387; Conservative 0; Mismatches 6; Indels 38; Gaps 2;

QY 1 MQALNTPQFSRLRDHNLTRQFIALYRLPLVYTPPLPGRKALVLTGLVFALAL 60
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Db 63 MQALNTTPEQFSKLLRDHNLTRQFIATYRLRPVUTPELPGRAKLALVLTGVLIFALAL 122
QY 61 FGNALFYVYVTRSKAMRTVNIIFICSLALSLLITPFCIPVTMLQNTSDNMLGGATICKM 120
Db 123 FGNALFYVYVTRSKAMRTVNIIFICSLALSLLITPFCIPVTMLQNTSDNMLGGATICKM 182
QY 121 VPFVQSTAVVTEILTWTCTIAVERHQGLVHPFKMKQWYTNRRRAFTMLGVVNLVAVIVGSPM 180
Db 183 VPFVQSTAVVTEILTWTCTIAVERHQGLVHPFKMKQWYTNRRRAFTMLGVVNLVAVIVGSPM 242
QY 181 WHVQQLLEIKYDFLYEKEHICCLBEWSPVHQKIYTTFFILVILFLPLMVMWLILYSKIGYE 240
Db 243 WHVQQLLEIKYDFLYEKEHICCLBEWSPVHQKIYTTFFILVILFLPLMVMWLILYSKIGYE 288
QY 241 LWTIKKAVGDSVLRTHIGKEMSKIARKKKAIVTMVTVVVALFAVCWAPFHVHMTLEYSN 300
Db 289 LW-----KKKRAVIMMVTVVVALFAVCWAPFHVHMTLEYSN 324
QY 301 FEKEYDDVTIKMIFAIQIIGFNSICNPVIYAFMNFKNVLSAVCYIVNKTSPAQ 360
Db 325 FEKEYDDVTIKMIFAIQIIGFNSICNPVIYAFMNFKNVLSAVCYIVNKTSPAQ 384
QY 361 RCGNSITWTKKAKKSLRNPEETKGEAFSDGNIIVKLCBOTEEKKKLKRHLALFRSE 420
Db 385 RCGNSITWTKKAKKSLRNPEETKGEAFSDGNIIVKLCBOTEEKKKLKRHLALFRSE 444
QY 421 LAENSPDLSGH 431
Db 445 LAENSPDLSGH 455

RESULT 2
Q8BHH0 PRELIMINARY; PRT; 365 AA.
AC Q8BHH0;
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DE Hypothetical rhodopsin-like GPCR superfamily containing protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Dorsal root ganglion, and Head;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium.
RA "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573 (2002).
DR EMBL; AK048439; BAC33337.1; -.
DR EMBL; AK051723; BAC34735.1; -.
KW Hypothetical protein.
SQ SEQUENCE 365 AA; 41759 MW; 1EB7E5369632ED56 CRC64;

Query Match 71.7%; Score 1603; DB 11; Length 365;
Best Local Similarity 81.3%; Pred. No. 1.3e-127;
Matches 305; Conservative 32; Mismatches 28; Indels 10; Gaps 3;

QY 53 VLIFALALFGNALVFVYVTRSKAMRTVNIIFICSLALSLLITPFCIPVTMLQNTSDNML 112
Db 1 MLIFALALFGNALVYVYVTRSKAMRTVNIIFICSLALSLLITPFCIPVTMLQNTSDNML 60
QY 113 GGAFICKMYPFVQSTAVVTEILTWTCTIAVERHQGLVHPFKMKQWYTNRRRAFTMLGVVNLV 172
Db 61 GGAFICKMYPFVQSTAVVTEILTWTCTIAVERHQGLVHPFKMKQWYTNRRRAFTMLGVVNLV 120
QY 173 AVIVGSPMWHVQQLLEIKYDFLYEKEHICCLBEWSPVHQKIYTTFFILVILFLPLMVMWL 232
Db 121 ALIIGSPMWHVQQLLEIKYDFLYEKEHICCLBEWSPVHQKIYTTFFILVILFLPLMVL 180

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QY 233 LYSKIGYELWIKKRVGDSVLRTHIGKEMSKIARKKKAIVTMVTVVVALFAVCWAPFHV 292
Db 181 LYSKIGYELWIKKRVGDSVLRTHIGKEMSKIARKKKAIVTMVTVVVALFAVCWAPFHV 240
QY 293 HMMIEYSNFEKEYDDVTIKMIFAIQIIGFNSICNPVIYAFMNFKNVLSAVCYIV 352
Db 241 HMMIEYSNFEKEYDDVTIKMIFAIQIIGFNSICNPVIYAFMNFKNVLSAVCYIV 300
QY 353 NKTSPAQRHGNSGTMMRKAKKSLRNPEETKGEAFSDGNIIVKLCBOTEEKKKLKR 412
Db 301 KETPSARHGSSGAMVWERRAKLAARENPV-EIKGEAFGGSNIDIKWCEQPEKKR--- 356
QY 413 HLAALFRSELAENSPL 427
Db 357 -----RSKVA-SCPL 365

RESULT 3
O57463 PRELIMINARY; PRT; 375 AA.
AC O57463;
DT 01-JUN-1998 (TRENBLrel. 06, Created)
DT 01-JUN-1998 (TRENBLrel. 06, Last sequence update)
DE Neuropeptide Y /peptide YY receptor Yb.
GN NPYRYB.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Lundell I., Berglund M.M., Starback P., Salaneck S., Gehlert D.R.,
RA Larhammar D.;
RT "Cloning and characterization of a novel neuropeptide Y (NPY) receptor
RT subtype in the zebrafish."
RL DNA Cell Biol. 0:0-0(1997);
DR EMBL; AF030245; AAB94616.1; -.
DR ZFIN; ZDB-GENE-980526-208; npyryb.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm1; 1.
DR PRINTS; PR00237; GPCRRHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 375 AA; 42116 MW; 4B0C9551131A14D1 CRC64;

Query Match 22.1%; Score 493.5; DB 13; Length 375;
Best Local Similarity 30.1%; Pred. No. 1.2e-33;
Matches 113; Conservative 79; Mismatches 142; Indels 41; Gaps 10;

QY 48 LVLGVLIFALALFGNALVFVYVTRSKAMRTVNIIFICSLALSLLITPFCIPVTMLQNI 107
Db 28 LIVAYSTMVAVGLVGNLCLVYVITRQKEMRNVTNIFVNLSCSDILVCLVLPVITVL 87
QY 108 SDNMLGGAFICKMYPFVQSTAVVTEILTWTCTIAVERHQGLVHPFKMKQWYTNRRRAFTMLG 167
Db 88 MDRWILGALCKVTPFVQSTAVVTEILTWTCTIAVERHQGLVHPFKMKQWYTNRRRAFTMLG 145
QY 168 VVNLVAVIVGSPMWHVQQL-----EIKYDFLYEKEHICCLBEWSPVHQKIYTTFFILVI 221
Db 146 VIWIIACFISLPFLSNILTNPSPHNLSPENPFSDFHICIEQWPSGEGNRITYTTITLLC 205
QY 222 LFLPLMVMWLILYSKIGYELWIKKRVGDSVLRTHIGKEMSKIARKKKAIVTMVTVVVAL 281
Db 206 QYCLFALILVCYFRIFLRLSRKDM---VERARGRQ--KKAKGSKRVNAMLASIVAA 259
QY 282 FAVCWAPFHVHMTLEYSNFEK----EYDDVTIKMIFAIQIIGFNSICNPVIYAFWNE 337
Db 260 FALCWPLNVENTITFDW-NHEAIPVQCHD-----AIFSACHLTAMASTCVNPVIYGFLLN 313
QY 338 NFKKNVLSAVCYIVNKTSPAQRHGNSGITMMRKAKKSLRNPEETKGEAFSDGNI 397

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Db 314 NFOKELKSLLSRC---RCWCPAESY-----ESFPLSTVSTGITKSLNSGSAS 359
Qy 398 VKLCEQTEKKKKR 412
Db 360 T---YQPHKKNLEQ 371

RESULT 4
Q924H0
ID Q924H0 PRELIMINARY; PRT; 417 AA.
AC Q924H0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Neuropeptide NPFF receptor.
GN NPFF
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RA Liu Q., Guan X.-M., McDonald T.P., Jiang Q., Zeng Z., Marlene J.,
RA Williams D.L. Jr., Hong Y., Figueroa D., Clements M.K., Mallee J.,
RA Wang R., Evans J., Gould R., Austin C.P.;
RT "Identification and characterization of two cognate receptors for
RT mammalian FMRFamide-like neuropeptides."
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AF330054; AAK94198.1; -.
DR MGD; MGI:1860130; Gpr74.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR InterPro; IPR005395; NPFF_receptor.
DR InterPro; IPR005397; NPFF_receptor2.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PRINTS; PR01570; NPFFRECEPTOR.
DR PRINTS; PR01572; NPFFRECEPTR2.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 417 AA; 47485 MW; AC0686514CDAF40C CRC64;

Query Match 21.7%; Score 485; DB 11; Length 417;
Best Local Similarity 31.0%; Pred. No. 7e-33;
Matches 121; Conservative 71; Mismatches 136; Indels 62; Gaps 11;

Qy 17 DHNLTRQFTALYRLRLPYTPPELPGRAKLALVLTGVLIFALALFGNALFYVYVTRSKAM 76
Db 29 DINIT---YVNYLHQPV-----AAVFSSYLLIFVLCWGVTVVCFIVIRNRHM 76
Qy 77 RTVTNIFICSLALSDLLITFCIPVTMLQNTSDNWLGAFTCKMVPFVQSTAVVTEILTM 136
Db 77 HTVTNFFILNLAISDLVIGIFCMPTLLDNIAGWPGSSMCKISGLVQGISVAASVFTL 136
Qy 137 TCIAVERHQGLVHPFKMKWYTNRRRAFTMLGVMLVAIVIGSP---MHWVQQLIKVDPL 193
Db 137 VAIAVDRPCVVPFKPK--LTVKTAFTVTVIINGLAINTPSAIMLHVQ--BEKYRV 192
Qy 194 YEKEH-----ICLEWTSVPVHOKIYTTFTILVFLPLMVMILYLSKIGYELWIKRV 247
Db 193 RLSSHNTSTVYWCREDWPRHEMRRIYTVLFTATYIPLSLIVIMYARIGASLP----- 247
Qy 248 GDGSLVLRTHGKMS---KTIARKKKRAVIMVTVVALFAVCWAPFHVHMMIEYSNEKE 304
Db 248 ---KTAHACTGKQRPQVQWHSKKQKVIKMLLTVALFILSWLPLMTIMLMSDYTDLSN 304
Qy 305 YDDVTIKMFAIVQIGFSNSICNPVYAFMNFENKKNVLSAVCYCIVNKTFSQAQRHGN 364
Db 305 KLRIINIYIPFAHLAFNCNSVNPITYGFNFENRFGQDAFOIC----- 350

Query Match 21.7%; Score 485; DB 11; Length 417;
Best Local Similarity 31.0%; Pred. No. 7e-33;
Matches 121; Conservative 71; Mismatches 136; Indels 62; Gaps 11;

Qy 17 DHNLTRQFTALYRLRLPYTPPELPGRAKLALVLTGVLIFALALFGNALFYVYVTRSKAM 76
Db 29 DINIT---YVNYLHQPV-----AAVFSSYLLIFVLCWGVTVVCFIVIRNRHM 76
Qy 77 RTVTNIFICSLALSDLLITFCIPVTMLQNTSDNWLGAFTCKMVPFVQSTAVVTEILTM 136
Db 77 HTVTNFFILNLAISDLVIGIFCMPTLLDNIAGWPGSSMCKISGLVQGISVAASVFTL 136
Qy 137 TCIAVERHQGLVHPFKMKWYTNRRRAFTMLGVMLVAIVIGSP---MHWVQQLIKVDPL 193
Db 137 VAIAVDRPCVVPFKPK--LTVKTAFTVTVIINGLAINTPSAIMLHVQ--BEKYRV 192
Qy 194 YEKEH-----ICLEWTSVPVHOKIYTTFTILVFLPLMVMILYLSKIGYELWIKRV 247
Db 193 RLSSHNTSTVYWCREDWPRHEMRRIYTVLFTATYIPLSLIVIMYARIGASLP----- 247
Qy 248 GDGSLVLRTHGKMS---KTIARKKKRAVIMVTVVALFAVCWAPFHVHMMIEYSNEKE 304
Db 248 ---KTAHACTGKQRPQVQWHSKKQKVIKMLLTVALFILSWLPLMTIMLMSDYTDLSN 304
Qy 305 YDDVTIKMFAIVQIGFSNSICNPVYAFMNFENKKNVLSAVCYCIVNKTFSQAQRHGN 364
Db 305 KLRIINIYIPFAHLAFNCNSVNPITYGFNFENRFGQDAFOIC----- 350

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Qy 365 SGITMRRKKAK----FSLR--ENPVEETKG 388
Db 351 -----QKXAKPOEAYSRLAKRNWINTSG 374

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RESULT 5

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Q8BXK6
ID Q8BXK6 PRELIMINARY; PRT; 417 AA.
AC Q8BXK6;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Neuropeptide NPFF receptor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RA SEQUENCE FROM N.A.
RA STRAIN=C57BL/6J; TISSUE=Body;
RA MEDLINE=22354683; PubMed=12466851;
RA The PANTOM Consortium.
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573(2002).
DR EMBL; AK050939; BAC34468.1; -.
SQ SEQUENCE 417 AA; 47449 MW; BB8D85E405D5786 CRC64;

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Query Match 21.7%; Score 485; DB 11; Length 417;
Best Local Similarity 30.8%; Pred. No. 7e-33;
Matches 120; Conservative 73; Mismatches 135; Indels 62; Gaps 11;

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Qy 17 DHNLTRQFTALYRLRLPYTPPELPGRAKLALVLTGVLIFALALFGNALFYVYVTRSKAM 76
Db 29 DINIT---YVNYLHQPV-----AAVFSSYLLIFVLCWGVTVVCFIVIRNRHM 76
Qy 77 RTVTNIFICSLALSDLLITFCIPVTMLQNTSDNWLGAFTCKMVPFVQSTAVVTEILTM 136
Db 77 HTVTNFFILNLAISDLVIGIFCMPTLLDNIAGWPGSSMCKISGLVQGISVAASVFTL 136
Qy 137 TCIAVERHQGLVHPFKMKWYTNRRRAFTMLGVMLVAIVIGSP---MHWVQQLIKVDPL 193
Db 137 VAIAVDRPCVVPFKPK--LTVKTAFTVTVIINGLAINTPSAIMLHVQ--BEKYRV 192
Qy 194 YEKEH-----ICLEWTSVPVHOKIYTTFTILVFLPLMVMILYLSKIGYELWIKRV 247
Db 193 RLSSHNTSTVYWCREDWPRHEMRRIYTVLFTATYIPLSLIVIMYARIGASLP----- 247
Qy 248 GDGSLVLRTHGKMS---KTIARKKKRAVIMVTVVALFAVCWAPFHVHMMIEYSNEKE 304
Db 248 ---KTAHACTGKQRPQVQWHSKKQKVIKMLLTVALFILSWLPLMTIMLMSDYTDLSN 304
Qy 305 YDDVTIKMFAIVQIGFSNSICNPVYAFMNFENKKNVLSAVCYCIVNKTFSQAQRHGN 364
Db 305 KLRIINIYIPFAHLAFNCNSVNPITYGFNFENRFGQDAFOIC----- 350

Query Match 21.7%; Score 485; DB 11; Length 417;
Best Local Similarity 30.8%; Pred. No. 7e-33;
Matches 120; Conservative 73; Mismatches 135; Indels 62; Gaps 11;

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RESULT 6

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Q9YHX1
ID Q9YHX1 PRELIMINARY; PRT; 374 AA.
AC Q9YHX1;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Neuropeptide Y-peptide YY receptor Yb.
GN NPYRB.
OS Gadus morhua (Atlantic cod).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Paracanthopterygii; Gadiformes; Gadidae; Gadus.
 OX NCBI_TaxID=8049;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99017378; PubMed=98023392;
 RA Arvidsson A.K., Wraith A., Jonsson-Rylander A.C., Larhammar D.;
 RT "Cloning of a neuropeptide Y/peptide YY receptor from the Atlantic
 RT cod: the Yb receptor";
 RL Regul. Pept. 75:39-43 (1998).
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 DR EMBL; AF073925; AAC02833.1; -;
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRHOOPS.
 DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS0262; G-PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Receptor; Transmembrane.
 SQ SEQUENCE 374 AA; 42260 MW; D2A9C9516C4998E2 CRC64;
 Query Match 21.7%; Score 484.5; DB 13; Length 374;
 Best Local Similarity 27.2%; Pred. No. 6.8e-33;
 Matches 108; Conservative 94; Mismatches 144; Indels 51; Gaps 10;
 QY 23 EQFI-----ALYRLPLVVTPELPGRAKLA---LVLTGVLIFALALFGNALVFYVVTSS 73
 Db 6 DQFINESHKPKANYSLQLAWDQECSPSSKSGTIFLIVYSTMAVGIVGNSCLVFIARQ 65
 QY 74 KMRVTNIFISLALSDLIITFCIPVTMLQNSDNWLGAPICKMVPFVQSTAVVTBI 133
 Db 66 KEMHNVNIFIANLSCDILMCFCLPVLTIYTMDRWILGKALCKLTFFVQCISVTVSI 125
 QY 134 LMTCTAVRHQGLVHPFKMKQYTNRAFTMLGVVLAVVAVGVSPWH-----VQO 185
 Db 126 FSLVLAMERYQIIILHP--TGWPKMVGQSTNAVGIIVWVACLISVPFLSTVLNDLPLQN 183
 QY 186 LEIKYDFLYEKEHICCLEWTSVPHQYITFTLILFLLPLMVLILSKIGYELWIKK 245
 Db 184 LSLPEP--GQDWLCTESWPTNSNRLAYTSLVQYFLPLGLIAACYLSIFLRLRRK 240
 QY 246 RVGDGSLVTIRGKENSKIARKKRAVIMVTVVALFVACWAPFHVHVMIEYSNFEKY 305
 Db 241 -----DMVERARDSSRDNRKASRRINVMVGSLVALFVACWLPNINFTVFDW-----H 289
 QY 306 DQVTI---KMIPAVQIIIGFNSICNPPIVAFMENFKKNVLSAVCYCIVNKTSPAPOR 361
 Db 290 HELMVSQHNLPFVCHLVAMASTCVNPPVYGFENSNFORQLKATLSHC---RCWGGAER 346
 QY 362 HGNSGITMMRKKAKFSLRENPNVEETKGEAFSDGNIEV 398
 Db 347 YENLPLSAV-----STEVTKEHMKSGSISI 372
 RESULT 7
 O73733
 ID O73733 PRELIMINARY; PRT; 377 AA.
 AC O73733;
 DT 01-AUG-1998 (TrEMBLrel. 07, Created)
 DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Neuropeptide Y/peptide YY receptor Ya.
 GN NPYRYA OR NPYRYA.
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98068842; PubMed=9407007;
 RA Lundell I., Berglund M.M., Starback P., Salaneck E., Gehlert D.R.,
 RA Larhammar D.;

RT "Cloning and characterization of a novel neuropeptide Y receptor
 RT subtype in the zebrafish";
 RL DNA Cell Biol. 16:1357-1363 (1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98096393; PubMed=9434780;
 RA Ringvall M., Berglund M.M., Larhammar D.;
 RT "Multiplicity of neuropeptide Y receptors: cloning of a third distinct
 RT subtype in the zebrafish";
 RL Biochem. Biophys. Res. Commun. 241:749-755 (1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99337783;
 RA Starback P., Lundell I., Fredriksson R., Berglund M.M., Yan Y.L.,
 RA Wraith A., Soderberg C., Postlethwait J.H., Larhammar D.;
 RT "Neuropeptide Y receptor subtype with unique properties cloned in the
 RT zebrafish: the zya receptor";
 RL Brain Res. Mol. Brain Res. 70:242-252 (1999).
 DR EMBL; AF037400; AAC41276.1; -;
 DR HSSP; P02699; 1F88.
 DR ZFIN; ZDB-GENE-980526-393; npyrya.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRHOOPS.
 DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS0262; G-PROTEIN_RECEP_F1_2; 1.
 KW Receptor.
 SQ SEQUENCE 377 AA; 42901 MW; 60562AD9C7BEE5D0 CRC64;
 Query Match 21.5%; Score 479.5; DB 13; Length 377;
 Best Local Similarity 29.7%; Pred. No. 1.8e-32;
 Matches 105; Conservative 83; Mismatches 131; Indels 35; Gaps 7;
 QY 46 LALVLTGVLIFALALFGNALVFVVTSSKAMRTVINIFISLALSDLIITFCIPVTMLQ 105
 Db 43 LTLVLCYCLVILGLLGNILLCIMHQRPDPNVTSLIANLSVDILVSVFCLPFTVY 102
 QY 106 NISDNWLGAPICKMVPFVQSTAVVTFTLTCTAVRHQGLVHPFKMKQYTNRAFTM 165
 Db 103 TMDHWIIGALLCLMLPFVQCVSTVSVLSVLIALERHQLILHP--SGWSPSVQAVIA 160
 QY 166 LGVWVLVAVIVGSPM--WH-----VQOLEIKYDFLYEKEHICCLEWTSVPVH 210
 Db 161 VLTWLLACVTSLSPLAFHLTTSBPSYSLFAPLSQLQV-----CLEVWPSQDH 208
 QY 211 QKIYVTFILVILFLLPLMVLILSKIGYELWIKKVGDSGLVLRTHGKENSKIARKKR 270
 Db 209 KLAYTTSLLLFQYCCPLLMILLCYLRIFLRQRRMLERQCSR--NEEDHRRVYMHSKR 266
 QY 271 AVIMVTVVALFVACWAPFHVHVMIEYSNFEKYDDV-TIKMIPAVQIIIGFNSICNP 329
 Db 267 INVMLATLVAFAVACWLPNANFVV---ADCDQEVLPVCNHNHLSLCHLLAMSTCVNP 323
 QY 330 IYAFPMENFKKNVLSAVCYCIVNKTSPAPORHGNISGITHMRKKAKFSLRENPNV 383
 Db 324 ILYGFENSNFRKDVASVVLHCHFPLEDSEYHFPMTMTNTDVSRTSFRLRNSV 377
 RESULT 8
 Q9ERC0
 ID Q9ERC0 PRELIMINARY; PRT; 381 AA.
 AC Q9ERC0;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Neuropeptide Y/peptide YY-Y2 receptor.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Wistar; TISSUE=Small intestine;

Qy	58	LALFQNALVYVYVTRSKAMRTVTNITFCSLAUSDLLITFTFCIPVTMTLQNSIDNWLGAFI	117
Db	53	LGIIVGNICLAIVARQKEKTNVTNIIISLIDFLMCLVCLPFTVYVYTMWDYWIFGEYM	112
Qy	118	CKWPFVFOSTAVVTETLMTCTCAVERSHQGLVHPFKMKQYTNRRFTMLGVVWLVAIVIG	177
Db	113	CKMTSFTOCTSVTSILSLVILALERHQIINP--TGMRPSSQAYGLGIVGWTIACLMS	170
Qy	178	SPMMHV-----QQLEIKYDFLYEKEHICCLEEWTSVPVHOKIYTTFTILVILFLLPLMV	229
Db	171	LPFLTTSILSNDLYEQLSHINNFSYDK--AICDSWPSQHRLLIYTTTLLLLQYCIPLFF	228
Qy	230	MLIYKIGYELWIKRVGDGSLRTTGKENSKIARKKKRAVIMVTVVVALFVCAWAPF	289
Db	229	IILCYLRIYLRLOKQKDMFEK-----EYSNRAVQLRRINILLASVAAFAVCWLP	280
Qy	290	HVHMMIBYSNFEKDYDDVTIKMIFAIQIIGFSNSICNPVYAFMNFKNVLSAVCY	349
Db	281	HVFNTIVDWN--YKILSPCHHNLIIFSLCHLVAMASTCVNPFVIGLNSNFKREVKSLLIS	338
Qy	350	CIVNKTFSQAQRHGNSGI--TMMRKKAKFTSLREN	381
Db	339	COHNSVTASIEDYDHLPLSTMOTGVSKGSLN	371
RESULT 11			
Q8BWV1		PRELIMINARY;	PRT; 381 AA.
ID	Q8BWV1		
AC	Q8BWV1		
DT	01-MAR-2003	(TremBLrel. 23, Created)	
DT	01-MAR-2003	(TremBLrel. 23, Last sequence update)	
DT	01-MAR-2003	(TremBLrel. 23, Last annotation update)	
DE	Neuropeptide Y receptor type 2.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=C57BL/6J; TISSUE=Hippocampus;		
RX	MEDLINE=22354683; PubMed=12466851;		
RA	the FANTOM Consortium,		
RA	the RIKEN Genome Exploration Research Group Phase I & II Team;		
RT	"Analysis of the mouse transcriptome based on functional annotation of		
RT	60,770 full-length cDNAs."		
RL	Nature 420:563-573 (2002).		
RQ	EMBL; AK049892; BAC33975.1; --		
SQ	SEQUENCE 381 AA; 42628 MW; 90787C051347884A CRC64;		

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Qy 322 FNSICNPVIYAFMNPENFKNVLSAVCYCIYNKTFSPAQR-----HGNSGITMMRKKAKPS 377
Db 315 MCSTFANPLLYGWMNSNYRKAFLSA-----FRCEQRDLTAIHSEVSMTFPAKK----- 361
Qy 378 LRENPVETKGEAPSDGNIQV 399
Db 362 -----NLEVK 366

RESULT 12
Q8BG12
ID O8BG12 PRELIMINARY; PRT; 460 AA.
AC O8EG12;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, last annotation update)
DE Orexin receptor type 2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1].
SEQUENCE FROM N.A.
RP RC STRAIN=C57BL/6J; TISSUE=Cerebellum, and Hypothalamus;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
DR EMEL; AK038851; BAC30039.1; -
DR EMEL; AK048781; BAC33457.1; -
SQ SEQUENCE 460 AA; 52461 MW; D62A67C15BA67DCC CRC64;

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RESULT 13

01-MAR-2003 (TrEMBLrel. 23, Created)
 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Neuropeptide Y receptor type 4.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 [1] _
 SEQUENCE FROM N.A.
 RP STRAIN=C57BL/6J; TISSUE=Urinary bladder;
 RC MEDLINE=22357BL6J; PubMed=12466851;
 RA The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573 (2002).
 DR EMBL; AK03505; BAC29082.1; --
 SQ SEQUENCE 375 AA; 42657 MW; 638BEA110E7F7A53 CRC64;

Query Match	20.2%;	Score 450.5;	DB 11;	Length 375;
Best Local Similarity	30.9%;	Pred. NO. 5.2e-30;		
Matches 98;	Conservative 72;	Mismatches 120;	Indels 27;	Gaps 8;

QY 46 LALVLFGVLI-PALALFGNALVFVVYTRSKAMRTVNIFICSLALSGLLITFFCIPVTML 104
 |||||::||::||::||::||::||::||::||::||::||::||:
 Db 41 LAFIITYTIEIILGVNLCLIFVTTROKESNVNTLLIANLAFSDFLMCLICQLPTLT 100
 |||||::||::||::||::||::||::||::||::||::||::||:

QY 105 QNISDNLGAGFCRMVPVQSTAVVTEILTMTCTIAVERHGVLHPFKMKWQYNRRRAFT 164
 |||||::||::||::||::||::||::||::||::||::||::||:
 Db 101 YTIMDYWFGEVKCKMKTIQCMSVTVSILSLVALERHQLINP--TGWKPSIFQAYL 158
 |||||::||::||::||::||::||::||::||::||::||::||:

QY 165 MLGVVMVLVAIVIGSP-----MHWVOOLETKYPDLYEKEHICGLEEWTSPHQKIYT 215
 |||||::||::||::||::||::||::||::||::||::||::||:
 Db 159 GIIVWTFVSCLSLPLANSTLNDLFYHNHVKV-VFLEDK--VVCFSWSSDHHLIIYT 215
 |||||::||::||::||::||::||::||::||::||::||::||:

QY 216 FTFLVLFLPLMWMLILYSKIGYLWIKRVRGDGSVLRTIHGKMSKIARKKKRAVINM 275
 |||||::||::||::||::||::||::||::||::||::||::||:
 Db 216 TELLFPQYCIPLAFLIVCYIRIVRHQRQKHV-----PHAACSSRAGOMKRINSML 267
 |||||::||::||::||::||::||::||::||::||::||::||:

QY 276 VTWVALFAVCAPFHVVHMNIEYSNPEKYDDVTIKMIPAIVOILGFNSICNPVIYAQM 335
 |||||::||::||::||::||::||::||::||::||::||::||:
 Db 268 MTMTVTAFAWLPLRVFTLEDW--YQEAI PACHGMLIFLMCHLLAWASTCVNPFYIGFL 325
 |||||::||::||::||::||::||::||::||::||::||::||:

QY 336 NFNFKNKLVSAV--CYC 350
 |||||::||::||::||::||::||::||::||::||::||::||:
 Db 326 NINFKKDIKALVLTCHC 342
 |||||::||::||::||::||::||::||::||::||::||::||:

RESULT 15
 QYVB87 PRELIMINARY; PRT; 449 AA.

ID QYVB87
 AC QYVB87;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE CS5811 protein.
 GN NEPYR OR CG5811.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Phyloroidea; Drosophilidae; Drosophila.
 NCBI_TaxID=7227;
 [1] _
 SEQUENCE FROM N.A.
 RP STRAIN=Berkelley;
 RC MEDLINE=20196006; PubMed=107311132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Calle R.F.,
 RA George R.A., Lewis S.B., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champes M., Pfeiffer B.D.,
 RA Wan X.H., Doyle C., Baxter P.G., Helt G., Nelson C.P., Millican G.J.,
 RN [1]

RA Abril J.F., Agbayani A., An H.-J., Andrews-Sfannkoch C., Baldwin D.,
 RA Bailew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Bertram P.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,
 RA Chertis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodok A., Gong F., Corvelli J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman I.J., Hernandez J.R., Houck J.,
 RA Hosain D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M.E., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshtina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kianos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,
 RA Evans C.A., Gocayne J.D., Anantides P.G., Brandon R.C., Rogers Y.,
 RA Banton J., An H., Baldwin D., Banston J., Beeson K.Y., Busam D.A.,
 RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
 RA Dodson K., Dorsett V., Doup L.B., Doyle C., Dresnek D., Farfan D.,
 RA Ferriera S., Frise E., Galle R.F., Garg N.S., George R.A.,
 RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
 RA Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
 RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,
 RA Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,
 RA Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
 RA Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,
 RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
 RT "Sequencing of *Drosophila melanogaster* genome.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
 RA Hradecky P., Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D.,
 RA Tupy J.I., Bergman C., Berman B., Carlson J.W., Celniker S.E.,
 RA Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
 RA Kronmiller B., Marshall B., Millburn C., Richter J., Russo S.,
 RA Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,
 RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
 RT "Annotation of *Drosophila melanogaster* genome.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RA FlyBase;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AE003759; AAF56655.2;
 DR FlyBase; Fgn0004842; Nery.
 DR InterPro; IPR000276; GPCR Rhodopsin.
 DR PRINTS; PR00237; GPCR RHODOPSIN.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.

DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
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 Best Local Similarity 28.4%; Pred. No. 1.7e-28;
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 DB 410 PALPLNRMTTSTTVISARRKPRATSLRANPL 440

Search completed: October 28, 2003, 10:14:00
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 28, 2003, 10:08:34 ; Search time 31 Seconds
(without alignments)
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Title: US-10-070-241B-1

Perfect score: 2235

Sequence: 1 MQALNITPQFSLLRDHNL.....RHLLFRSELAENSLDLSGH 431

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 629382 seqs, 167460630 residues

Total number of hits satisfying chosen parameters: 629382

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
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- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2235	100.0	431	9	US-09-826-508-22
2	2235	100.0	431	9	US-09-899-532-2
3	2235	100.0	431	11	US-09-990-940-6
4	2232	99.9	431	12	US-10-272-983-38
5	2232	99.9	431	12	US-10-393-807-38
6	2135	95.5	415	12	US-10-080-263C-2
7	1914	85.5	433	11	US-09-990-940-16
8	1767	79.1	416	11	US-09-990-940-18
9	1268	56.7	245	15	US-10-225-567A-510
10	579	25.9	179	12	US-10-017-161-1154
11	502	22.5	420	10	US-09-866-248A-6
12	501.5	22.4	420	12	US-10-060-369-9
13	501.5	22.4	522	15	US-10-225-567A-512
14	479	21.4	381	12	US-10-188-619-4
15	479	21.4	381	15	US-10-067-649-5

16	474	21.2	381	12	US-10-188-619-6	Sequence 6, Appl
17	469.5	21.0	381	10	US-09-962-646-16	Sequence 16, Appl
18	469.5	21.0	381	10	US-09-292-973-5	Sequence 5, Appl
19	469.5	21.0	381	10	US-09-292-973-20	Sequence 20, Appl
20	469.5	21.0	381	12	US-10-188-619-2	Sequence 2, Appl
21	469.5	21.0	381	15	US-10-225-567A-201	Sequence 201, App
22	466.5	20.9	385	11	US-09-992-331-18	Sequence 18, Appl
23	466.5	20.9	385	16	US-10-262-313-18	Sequence 18, Appl
24	455	20.4	444	11	US-09-992-331-19	Sequence 19, Appl
25	455	20.4	444	12	US-10-060-369-11	Sequence 11, Appl
26	455	20.4	444	12	US-10-178-194-2	Sequence 2, Appl
27	455	20.4	444	15	US-10-225-567A-370	Sequence 370, App
28	455	20.4	444	16	US-10-262-313-19	Sequence 19, App
29	453	20.3	444	15	US-10-282-717-2	Sequence 2, Appl
30	440.5	19.7	385	12	US-10-359-285-5	Sequence 5, Appl
31	440	19.7	385	15	US-10-067-649-6	Sequence 6, Appl
32	437	19.6	432	10	US-09-866-248A-2	Sequence 2, Appl
33	434.5	19.4	432	12	US-10-254-905-9	Sequence 9, Appl
34	434.5	19.4	348	11	US-09-966-782A-9	Sequence 9, Appl
35	433.5	19.4	464	12	US-10-283-423-14	Sequence 14, Appl
36	433.5	19.4	464	12	US-10-213-821-14	Sequence 14, Appl
37	432.5	19.4	428	10	US-09-292-973-4	Sequence 4, Appl
38	432.5	19.4	430	10	US-09-866-248A-8	Sequence 8, Appl
39	432.5	19.4	430	15	US-10-225-567A-658	Sequence 658, App
40	431.5	19.3	345	12	US-10-254-905-10	Sequence 10, Appl
41	431.5	19.3	345	16	US-10-262-313-11	Sequence 11, Appl
42	431.5	19.3	346	8	US-08-899-112-32	Sequence 32, Appl
43	431.5	19.3	346	11	US-09-966-782A-10	Sequence 10, Appl
44	431.5	19.3	346	11	US-09-992-331-11	Sequence 11, Appl
45	431.5	19.3	346	11	US-09-771-287-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1
US-09-826-508-22
; Sequence 22, Application US/09826508
; Patent No. US20010025099A1
; GENERAL INFORMATION:
; APPLICANT: Nabil Elshourbagy
; APPLICANT: Lisa Vawter
; TITLE OF INVENTION: G Protein-Coupled Receptor Polypeptides
; TITLE OF INVENTION: and Polynucleotides
; FILE REFERENCE: GP-70744USB
; CURRENT APPLICATION NUMBER: US/09/826,508
; CURRENT FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 431
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-826-508-22

Query Match	100.0%;	Score	2235;	DB	9;	Length	431;
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Gaps	0;						
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Db	181	WHVQQLLEIKYDFLYEKEHICCLLEWTSVHQKIYTTFTILVILFLPLMVMVLLYSKIGYE	240				

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Db 361 RHNSGITMWRKAKFSLRENPEETKGEAFSDGNI EVKLCBOTBEKKLKRHLALFRSE 420
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Db 421 LAENSPDLSGH 431

RESULT 2
US-09-899-532-2
; Sequence 2, Application US/09899532
; Patent No. US20020048791A1
; GENERAL INFORMATION:
; APPLICANT: Bloomquist, Brian T.
; APPLICANT: Zhelnin, Leonid
; TITLE OF INVENTION: Human Neuropeptide Y-Like G
; TITLE OF INVENTION: Protein-Coupled Receptor
; FILE REFERENCE: 02973.00040
; CURRENT APPLICATION NUMBER: US/09/899,532
; CURRENT FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: US 60/216,523
; PRIOR FILING DATE: 2000-07-06
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-899-532-2

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Best Local Similarity 100.0%; Pred. No. 1.7e-194;
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QY 421 LAENSPDLSGH 431
Db 421 LAENSPDLSGH 431
RESULT 3
US-09-990-940-6
; Sequence 6, Application US/09990940
; Publication No. US20030027252A1
; GENERAL INFORMATION:
; APPLICANT: Tian, Hui
; APPLICANT: Zhao, Jiagang
; APPLICANT: Chen, Jin-Long
; APPLICANT: Cutler, Gene
; APPLICANT: An, Songzhu
; APPLICANT: Dai, Kang
; APPLICANT: Gupta, Jamila S.
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: No. US20030027252A1e1 Receptors
; FILE REFERENCE: 018781-007410US
; CURRENT APPLICATION NUMBER: US/09/990,940
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/252,841
; PRIOR FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: US 60/257,636
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 60/261,377
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 60/279,554
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 60/280,696
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human G-protein coupled receptor (GPCR) TGR346
US-09-990-940-6

Query Match 100.0%; Score 2235; DB 11; Length 431;
Best Local Similarity 100.0%; Pred. No. 1.7e-194;
Matches 431; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 FGNALVFYVTVTRSKAMRTVTNIFICSALSDLLITFFCIPVTMLQNSDNLGGAFICKM 120
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 DB 421 LAENSPDLSGH 431
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 ; Sequence 38, Application US/10272983
 ; Publication No. US20030148450A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Chen, Ruoping
 ; APPLICANT: Dang, Huong T.
 ; APPLICANT: Liaw, Chen W.
 ; APPLICANT: Lin, I-Lin
 ; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
 ; FILE REFERENCE: AREN0050
 ; CURRENT APPLICATION NUMBER: US/10/272,983
 ; CURRENT FILING DATE: 2002-10-17
 ; PRIOR APPLICATION NUMBER: US/09/417,044
 ; PRIOR FILING DATE: 1999-10-12
 ; PRIOR APPLICATION NUMBER: 60/109,213
 ; PRIOR FILING DATE: 1998-11-20
 ; PRIOR APPLICATION NUMBER: 60/120,416
 ; PRIOR FILING DATE: 1999-02-16
 ; PRIOR APPLICATION NUMBER: 60/121,951
 ; PRIOR FILING DATE: 1999-02-26
 ; PRIOR APPLICATION NUMBER: 60/123,946
 ; PRIOR FILING DATE: 1999-03-12
 ; PRIOR APPLICATION NUMBER: 60/123,949
 ; PRIOR FILING DATE: 1999-03-12
 ; PRIOR APPLICATION NUMBER: 60/136,436
 ; PRIOR FILING DATE: 1999-05-28
 ; PRIOR APPLICATION NUMBER: 60/136,437
 ; PRIOR FILING DATE: 1999-05-28
 ; PRIOR APPLICATION NUMBER: 60/136,439
 ; PRIOR FILING DATE: 1999-05-28
 ; PRIOR APPLICATION NUMBER: 60/136,567
 ; PRIOR FILING DATE: 1999-05-28
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 74
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 38
 ; LENGTH: 431
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-272-983-38
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 Best Local Similarity 99.8%; Pred. No. 3.2e-194;
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 QY 1 MQALNITPEQSLRDHNLTRQFIYALYRLPLVYTPPELGRKALVLTGVLFALAL 60
 DB 1 MQALNITPEQSLRDHNLTRQFIYALYRLPLVYTPPELGRKALVLTGVLFALAL 60
 QY 61 FGVALVFYVYVTRSKAMRTVTNIFICSLSLSDLLITFFCIPVTMLQNSDNWLGGAFCIKM 120
 DB 61 FGVALVFYVYVTRSKAMRTVTNIFICSLSLSDLLITFFCIPVTMLQNSDNWLGGAFCIKM 120
 QY 121 VPFVQSTAVVTEILMTWCIAVERHQGLVHPFKMKQWYTNRRRAFTMLGVVWLVAIVGSPM 180
 DB 121 VPFVQSTAVVTEILMTWCIAVERHQGLVHPFKMKQWYTNRRRAFTMLGVVWLVAIVGSPM 180
 QY 181 WHVQOLEIKYDFLYEKHEHCLEBWSVPHQKIYTTFFILVILFLPLVMMLILYSKIGYE 240
 DB 181 WHVQOLEIKYDFLYEKHEHCLEBWSVPHQKIYTTFFILVILFLPLVMMLILYSKIGYE 240
 QY 241 LWIKKRVGDSGLVLRTHGKEMSLIARKKRAVIMVTVVALFAVCWAPHHVHHMIEYSN 300
 DB 241 LWIKKRVGDSGLVLRTHGKEMSLIARKKRAVIMVTVVALFAVCWAPHHVHHMIEYSN 300
 QY 301 FEKEYDDVTIKMFAIVQIIGFSSNCNPIYAFNENFKKNVLSAVCYCIVNKTFSPAQ 360

Db 421 LSENSTFGSGH 431

RESULT 8
US-09-990-940-18
; Sequence 18, Application US/09990940
; Publication No. US20030027252A1
; GENERAL INFORMATION:
; APPLICANT: Tian, Hui
; APPLICANT: Zhao, Jiagang
; APPLICANT: Chen, Jin-Long
; APPLICANT: Cutler, Gene
; APPLICANT: An, Songzhu
; APPLICANT: Dai, Kang
; APPLICANT: Gupte, Jamila S.
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: No. US20030027252A1el Receptors
; FILE REFERENCE: 018781-007410US
; CURRENT APPLICATION NUMBER: US/09/990,940
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/252,841
; PRIOR FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: US 60/257,636
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 60/261,377
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 60/279,554
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 60/280,696
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 18
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Mus sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1302)
; OTHER INFORMATION: mouse G-protein coupled receptor (GPCR) TGR346b

US-09-990-940-18
Query Match 79.1%; Score 1767; DB 11; Length 416;
Best Local Similarity 80.1%; Pred. No. 4.9e-152;
Matches 339; Conservative 36; Mismatches 38; Indels 10; Gaps 3;

Qy 5 NITPEQSLRLDNLNLTREQIALYRLPLVYTBELPGRKALVLTGLPALALFQNA 64
Db 4 NLTAEQSALLRLNLTQRAQFIHYGRPLVTPQLPARALALLVGLLIFALALFQNA 63
Qy 65 LVFVVTNRKAMRTVTNIFICSLALSLLIIFFCIPVTMLQNISDNMLGGAFICKMVPFV 124
Db 64 LVVVTNRKAMRTVTNIFICSLALSLLIIFFCIPVTMLQNVSDTNLGGAFICKMVPFV 123
Qy 125 QSTAVVTETLMTCTIAVERHOGLVHPFKQKQYNRRFTMLGVVWLVAVTVGSPMHRVQ 184
Db 124 QCTAIVTEILTMTCTIAVERHOGLVHPFKQKQYNRRFTMLGVVWLVAVTVGSPMHRVQ 183
Qy 185 QLEIKYDPLYEKEHCCLLEWTSVPHQKIYTFILVILFLLPLMVLILYSKIGYELWIK 244
Db 184 RLEIKYDPLYEKEHCCLLEWTSVPHQKIYTFILVILFLLPLMVLILYSKIGYELWIK 243
Qy 245 KRVDGSGVLRITIHGKEMSKIARKKKRAVIMVTVVVALFAVCWAPPHVVMHMIYSNFEKE 304
Db 244 KRIGDGSVLRITIHGKEMSKIARKKKRAVIMVTVVVALFAVCWAPPHVVMHMIYSNFEKE 303
Qy 305 YDDVTIKMIFAIVQIIGFSNSICNPVYAFNENFKKNVL SAVCYCIVNKTFTSPAQRHGN 364
Db 304 YDEVTKMIFAIVQIIGFSNSICNPVYAFNENFKKNVL SAVCYCIVNKTFTSPAQRHGS 363
Qy 365 SGIITMRKKAFFSRENPVEETKGEAFSDGNIEVKLCBOTEEKKKLKHLLALFRSELAEN 424
Db 364 SGAMVMMHRRKLAARENVP-BIKGEAFGGSNIDIKWCQEPEKKXR-----RSKVA-S 413

Qy 425 SPL 427
Db 414 CPL 416

RESULT 9
US-10-225-567A-510
; Sequence 510, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTOR
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 510
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-510

Query Match 56.7%; Score 1268; DB 15; Length 245;
Best Local Similarity 99.2%; Pred. No. 4.8e-107;
Matches 243; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 186 LEIKYDPLYEKEHCCLLEWTSVPHQKIYTFILVILFLLPLMVLILYSKIGYELWIK 245
Db 1 MKLYDPLYEKEHCCLLEWTSVPHQKIYTFILVILFLLPLMVLILYSKIGYELWIK 60
Qy 246 RVGDGSGVLRITIHGKEMSKIARKKKRAVIMVTVVVALFAVCWAPPHVVMHMIYSNFEKE 305
Db 61 RVGDGSGVLRITIHGKEMSKIARKKKRAVIMVTVVVALFAVCWAPPHVVMHMIYSNFEKE 120
Qy 306 DDVTIKMIFAIVQIIGFSNSICNPVYAFNENFKKNVL SAVCYCIVNKTFTSPAQRHGS 365
Db 121 DDVTIKMIFAIVQIIGFSNSICNPVYAFNENFKKNVL SAVCYCIVNKTFTSPAQRHGS 180
Qy 366 GITMRKKAFFSRENPVEETKGEAFSDGNIEVKLCBOTEEKKKLKHLLALFRSELAENS 425
Db 181 GITMRKKAFFSRENPVEETKGEAFSDGNIEVKLCBOTEEKKKLKHLLALFRSELAENS 240
Qy 426 PLDSG 430
Db 241 PLDSG 245

RESULT 10
US-10-017-161-1164
; Sequence 1164, Application US/10017161
; Publication No. US20030143668A1
; GENERAL INFORMATION:
; APPLICANT: SUWA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ABURATANI, HIROVUKI
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 084335/0152
; CURRENT APPLICATION NUMBER: US/10/017,161
; CURRENT FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: JP 2001/246789
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 2430
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 1164
; LENGTH: 179

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-017-161-1164

Query Match      25.9%; Score 579; DB 12; Length 179;
Best Local Similarity 73.6%; Pred. No. 1.1e-44;
Matches 120; Conservative 10; Mismatches 13; Indels 20; Gaps 2;

QY 1 MQALNITPQFSRLRDHNLTEQFIALYRLRPLVYTPPELPGRAKLALVLTGVLIFALAL 60
DB 1 MQALNITPQFSRLRDHNLTEQFIALYRLRPLVYTPPELPGRAKLALVLTGVLIFALAL 60
QY 61 FGNALVYVYVTSKAMRTVTNIFICSALSDLLITFFCIPVTMLQNISDNWLG----- 114
DB 61 FGNALVYVYVTSKAMRTVTNIFICSALSDLLITFFCIPVTMLQNISDNWLGKSRAPL 120
QY 115 --AFICKMVPF-----VQSTAVVTELTMTCTAVER 143
DB 121 LRSFSLNPLPFRGSLSLSLSLSLSLSLSLSLSLSLSLSLSLSLSLSLSLSLSLS 163

RESULT 11
US-09-866-248A-6
; Sequence 6, Application US/09856248A
; Publication No. US20020198367A1
; GENERAL INFORMATION:
; APPLICANT: Gerald, Christophe P.G.
; APPLICANT: Jones, Kenneth A.
; APPLICANT: Bonini, James A.
; APPLICANT: Borowsky, Beth
; TITLE OF INVENTION: DNA Encoding Mammalian Neuropeptide PF (NPFF) Receptors
; FILE REFERENCE: 1795/57155-A
; CURRENT APPLICATION NUMBER: US/09/866,248A
; PRIOR FILING DATE: 2001-05-25
; PRIOR FILING DATE: 09/161,113
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: Patent In Ver. 2.0 - beta
; SEQ ID NO 6
; LENGTH: 420
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-866-248A-6

Query Match      22.5%; Score 502; DB 10; Length 420;
Best Local Similarity 30.1%; Pred. No. 3.2e-37;
Matches 128; Conservative 87; Mismatches 162; Indels 48; Gaps 12;

QY 14 LLDHNLTEQFIALYRLRPLVYTPPELPGRAKLALVLTGVLIFALALFGNALVYVYVTS 73
DB 26 LYSDNIT---YVNYLHQPV-----AAFIISYFLIFFLCMGNTVVCFTVMEN 73
QY 74 KAMRTVTNIFICSALSDLLITFFCIPVTMLQNISDNWLGAFICKMVPFVQSTAVVTEI 133
DB 74 KMHVTVNLFILNALSDLLVGFICMPTLLDNIAGWFFGNTWCKISGLVQGISVAASV 133
QY 134 LTMCTIAVERHOGLVHPFKMKQYTNRRAPTMGLGVVVLVAVIVGSP---MHHVQQLLEIKY 190
DB 134 FTLVAIAVDREFQCVVYFPKP--LTIKTAFVIIMIWLAITIMSPSAVMLHVQ--EKY 190
QY 191 DFLYEKEH-----ICCLEWTSVHOKIYTTFTLVILFLLPLMVMMLIYSKIGYELWIKK 245
DB 191 RVLNSQNTSPVYWCREDWPNQEMRKIYTVTLFANIYLAFLSLIVIMYGRIGISLF--- 247
QY 246 RVGDSGLVRLTHGKEMSK---IARKKRAVIMVTVVVALFAVCWAPPHVVMHMEIYSNF 301
DB 248 ---RAAVPHT--GRKQEQHVSVRKKQKIIMLLIALLFILSLPLMTLMLSDYADL 302
QY 302 EKEYYDDVTIKMFAIVQIIGFSNSICNPVIYAFNENFKKNVLSAVCYCIANKTSPAQ 361
DB 303 SPNELQIINIYIYPPAHWLAFGNSSVNPFIYGFNENFRGRGQEAFLQLCQKRAKPM 362

RESULT 12
US-10-060-369-9
; Sequence 9, Application US/10060369
; Publication No. US20030139589A1
; GENERAL INFORMATION:
; APPLICANT: Zastawny, Roman
; TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR A4
; FILE REFERENCE: 2931-104
; CURRENT APPLICATION NUMBER: US/10/060,369
; PRIOR FILING DATE: 2003-03-31
; PRIOR FILING DATE: 1998-08-16
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patent In version 3.2
; SEQ ID NO 9
; LENGTH: 420
; TYPE: PRT
; ORGANISM: Human
US-10-060-369-9

Query Match      22.4%; Score 501.5; DB 12; Length 420;
Best Local Similarity 30.1%; Pred. No. 3.5e-37;
Matches 124; Conservative 83; Mismatches 142; Indels 63; Gaps 12;

QY 14 LLDHNLTEQFIALYRLRPLVYTPPELPGRAKLALVLTGVLIFALALFGNALVYVYVTS 73
DB 26 LYSDNIT---YVNYLHQPV-----AAFIISYFLIFFLCMGNTVVCFTVMEN 73
QY 74 KAMRTVTNIFICSALSDLLITFFCIPVTMLQNISDNWLGAFICKMVPFVQSTAVVTEI 133
DB 74 KMHVTVNLFILNALSDLLVGFICMPTLLDNIAGWFFGNTWCKISGLVQGISVAASV 133
QY 134 LTMCTIAVERHOGLVHPFKMKQYTNRRAPTMGLGVVVLVAVIVGSP---MHHVQQLLEIKY 190
DB 134 FTLVAIAVDREFQCVVYFPKP--LTIKTAFVIIMIWLAITIMSPSAVMLHVQ--EKY 190
QY 191 DFLYEKEH-----ICCLEWTSVHOKIYTTFTLVILFLLPLMVMMLIYSKIGYELWIKK 245
DB 191 RVLNSQNTSPVYWCREDWPNQEMRKIYTVTLFANIYLAFLSLIVIMYGRIGISLF--- 247
QY 246 RVGDSGLVRLTHGKEMSK---IARKKRAVIMVTVVVALFAVCWAPPHVVMHMEIYSNF 301
DB 248 ---RAAVPHT--GRKQEQHVSVRKKQKIIMLLIALLFILSLPLMTLMLSDYADL 302
QY 302 EKEYYDDVTIKMFAIVQIIGFSNSICNPVIYAFNENFKKN---IARKKRAVIMVTVVVALFAVCWAPPHVVMHMEIYSNF 301
DB 303 SPNELQIINIYIYPPAHWLAFGNSSVNPFIYGFNENFRGRGQEAFLQLCQKRAKPM 362

RESULT 13
US-10-225-567A-512
; Sequence 512, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Glenn C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTOR
; FILE REFERENCE: 1920-4-4
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; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 512
; LENGTH: 522
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-512

Query Match      22.4%; Score 501.5; DB 15; Length 522;
Best Local Similarity 30.1%; Pred. No. 4.6e-37;
Matches 124; Conservative 83; Mismatches 142; Indels 63; Gaps 12;

QY 14 LLDHNLTRQFIALYRLRLVYTPPELPGRAKLALVTGLVIFALFGLNALFVYVTR 73
Db 128 LYSIDNIT---VYNYLHQPV-----AAFIISYFLIFLCLMNGNTVVCFIVMRN 175

QY 74 KAMRTVTNIFICSLSLSDLIITFCIPVTMLQNSDNLGAFICKVVPFVQSTAVVTEI 133
Db 176 KHMHTVTNLFILNALISDLVGLVFCMPITLLDNLIAAGPPGNTWCKISGLVQGISVAASV 235

QY 134 LTMCTIAVERHQGLVHPFKMKQYTNRRRAFTMLGVWMLVAVIVGSP---MWHVQOLEIKY 190
Db 236 FTLVAIAVDFQCVVYFPEK--LTIKTAFTVIMIIWLAITNSPAVMLHQE-EKYY 292

QY 191 DFLYEKEH-----ICCLBEWTSVHQKIYTFILVILFLPLMWMLILYKIGVELMIKK 245
Db 293 RVRINSQNKTSPPVYWCREDPNQEMRKIYTTVFLFANILYPLSLIVIMYGRIGSLP--- 349

QY 246 RVGDSVLRITGHKEMSK---IARKKKRAVIMVMTVVALFVAVCWAPPHVVMHIEYSNF 301
Db 350 ---RAAVPHT--GRNQEOMHVVRKKQKIIMLLIIVALLFILSLWPLNLMUSDYADL 404

QY 302 EKEYDDVTIKMFAIVQIIGFSNICSNPVIYAFNENFKKN----- 342
Db 405 SPNELQIINIVYPPFAHLAFNGSSVNPPIIYGFNENFRGFEAFQOLQCRKAPMEA 464

QY 343 -VLSAVCYIVNKTFSAPQ-----HGNSGITMWRKAKESLRENPEVETK 387
Db 465 YTLKAKSHVLINTSNQLVQESTFQNPGET--LLYRKSAEKPOQELVMEELK 514

RESULT 14
US-10-188-619-4
; Sequence 4, Application US/10188619
; Publication No. US20030162944A1
; GENERAL INFORMATION:
; APPLICANT: Christophe P.G. Gerald, et al.
; TITLE OF INVENTION: METHOD OF OBTAINING COMPOSITIONS COMPRISING Y2
; TITLE OF INVENTION: SPECIFIC COMPOUNDS
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESS: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/188,619
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/407,367
; FILING DATE:

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; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 44742-AA-PCT-US/JPW
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 381 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-10-188-619-4

Query Match      21.4%; Score 479; DB 12; Length 381;
Best Local Similarity 29.9%; Pred. No. 3.4e-35;
Matches 120; Conservative 78; Mismatches 144; Indels 60; Gaps 12;

QY 17 DHNLTRQFIALYRLRLVYTPPELPG-----RAKLALVTGLVIFALFGLN 63
Db 9 DENQTVKVELYSGSPTTPRGELPPDPPELIDSTKLVEVQVLLAYCSIIILGVVGN 68

QY 64 ALVYVTVTRSKAMRTVTNIFICSLSLSDLIITFCIPVTMLQNSDNLGAFICKVVPF 123
Db 69 SLVHVIVIKFSKRTVTNFIANLAVADLLVNTLCLPFTLTITLMGEWKNQGPVLCHLPY 128

QY 124 VQSTAVTEILTMCTIAVERHQGLVHPFKMKQYTNRRRAFTMLGVWMLVAVIVGSPMWHV 183
Db 129 AQGLAVQVSTITLTIADLRHCIVVHLESK--ISKQISFLITGLANGVSALLASPLAIF 186

QY 184 QQ---LEIKYDFLYEKEHICCLEEM--TSPVHOKIYTTFILVILFLPLMWMLILYSKI 237
Db 187 REYSLIEILPDF---EIVACTEKWGEKSVYGVTSLSLTLVYLPLIGIISFSVTRI 242

QY 238 GYELW--IKRVGDGSLRLTIHGKEMSKIAKKRAVIMVMTVVALFVAVCWAPPHVVMH 295
Db 243 ---WSKLNHVSPGAASDHYH-----QRRHKTTKMLVCVVVWFAVSWLPLHAFOLA 290

QY 296 IEYSNFE---KEYDDVTIKMFAIVQIIGFSNICSNPVIYAFNENFKKNVLSAVCYIV 352
Db 291 VDISHVLDLKEY-----KLIFTVFHIIAMCSTFANPLLYGWNMSNYRKAPLSA----- 339

QY 353 NKTFSAPQ---HGNSGITMWRKAKESLRENPEVETKGEA 390
Db 340 ---FRCEQLDAIHSEVSWTTPKAKNLEVKKNGLDTSFSEA 378

RESULT 15
US-10-067-649-5
; Sequence 5, Application US/10067649
; Publication No. US20030100057A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBMV14, RELATED TO
; TITLE OF INVENTION: ORPHAN GPCR, GPR73
; FILE REFERENCE: D0118 NP
; CURRENT APPLICATION NUMBER: US/10/067,649
; CURRENT FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: US 60/266,525
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: US 60/329,897
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 5
; LENGTH: 381
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-067-649-5

Query Match      21.4%; Score 479; DB 15; Length 381;
Best Local Similarity 29.9%; Pred. No. 3.4e-35;

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OM nucleic - nucleic search, using sw model

Run on: October 29, 2003, 07:53:00 ; Search time 654 Seconds
(without alignments)

10043.271 Million cell updates/sec

Title: US-10-070-241B-2

Perfect score: 2415

Sequence: 1 gccagagcgccaggaccct.....aaaaaaaaaaaaaaaaaagg 2415

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1811591 seqs, 1359896290 residues

Total number of hits satisfying chosen parameters: 3623182

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA.*

- 1: /cgn2_6/ptodata/1/pubnpa/US07_PUBCOMB.seq.*
- 2: /cgn2_6/ptodata/1/pubnpa/PCT_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/1/pubnpa/US06_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/1/pubnpa/US06_PUBCOMB.seq.*
- 5: /cgn2_6/ptodata/1/pubnpa/US07_NEW_PUB.seq.*
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- 10: /cgn2_6/ptodata/1/pubnpa/US09B_PUBCOMB.seq.*
- 11: /cgn2_6/ptodata/1/pubnpa/US09C_PUBCOMB.seq.*
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- 13: /cgn2_6/ptodata/1/pubnpa/US10A_PUBCOMB.seq.*
- 14: /cgn2_6/ptodata/1/pubnpa/US10B_PUBCOMB.seq.*
- 15: /cgn2_6/ptodata/1/pubnpa/US10_NEW_PUB.seq.*
- 16: /cgn2_6/ptodata/1/pubnpa/US60_NEW_PUB.seq.*
- 17: /cgn2_6/ptodata/1/pubnpa/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1668.4	69.1	1710	9	US-09-899-532-3
2	1495	61.9	1495	12	US-10-080-263C-1
3	1296	53.7	1296	9	US-09-826-508-21
4	1296	53.7	1296	9	US-09-899-532-1
5	1296	53.7	1296	11	US-09-990-940-5
6	1294.4	53.6	1296	12	US-10-272-983-37
7	1294.4	53.6	1296	12	US-10-393-807-37
8	1078.4	44.7	1368	14	US-10-225-567A-509
9	994.6	41.2	1737	11	US-09-990-940-15
10	932	38.6	1772	11	US-09-990-940-17
11	542	22.4	940	12	US-10-017-161-1163
12	500	20.7	511	12	US-10-272-983-45
13	500	20.7	511	12	US-10-393-807-45
14	309	12.8	432	9	US-09-812-102-73
15	251.4	10.4	114793	12	US-10-148-806-3
16	249.8	10.3	31871	10	US-09-764-847-1403

17	249.8	10.3	31871	14	US-10-092-154-1403	Sequence 1403, Ap
18	249.6	10.3	288	12	US-10-229-058B-14	Sequence 14, Appl
19	249.2	10.3	684973	10	US-09-263-959-1	Sequence 1, Appli
20	248.4	10.3	250000	12	US-10-225-810-26	Sequence 26, Appl
21	248	10.3	1538	13	US-10-027-632-259313	Sequence 259313,
c 22	247.8	10.3	31474	11	US-09-764-891-8149	Sequence 8149, Ap
c 23	247.6	10.3	300000	14	US-10-262-552-33	Sequence 33, Appl
24	247.4	10.2	11360	11	US-09-764-891-6508	Sequence 6508, Ap
25	247.4	10.2	11360	11	US-09-764-891-7415	Sequence 7415, Ap
26	246.8	10.2	1538	13	US-10-027-632-259314	Sequence 259314,
27	246.8	10.2	1538	13	US-10-027-632-259315	Sequence 259315,
c 28	246	10.2	203654	10	US-09-820-905-3	Sequence 3, Appli
c 29	245.6	10.2	1400	10	US-09-263-959-295	Sequence 295, App
c 30	245.6	10.2	35465	14	US-10-161-572-6	Sequence 6, Appli
c 31	245.6	10.2	36991	14	US-10-161-572-8	Sequence 8, Appli
c 32	245.6	10.2	684973	10	US-09-263-959-1	Sequence 1, Appli
33	245.6	10.2	1691139	14	US-10-067-514-1	Sequence 1, Appli
34	245.4	10.2	119596	14	US-10-270-336-3	Sequence 3, Appli
35	245.2	10.2	378361	11	US-09-901-136-3	Sequence 3, Appli
c 36	244.6	10.1	3512	13	US-10-027-632-114278	Sequence 114278,
c 37	244.6	10.1	3512	13	US-10-027-632-114279	Sequence 114279,
c 38	244.4	10.1	618	13	US-10-027-632-281878	Sequence 281878,
39	244	10.1	1701	13	US-10-027-632-264344	Sequence 264344,
40	244	10.1	1701	13	US-10-027-632-264345	Sequence 264345,
41	244	10.1	1701	13	US-10-027-632-264346	Sequence 264346,
42	244	10.1	1701	13	US-10-027-632-264347	Sequence 264347,
43	244	10.1	1701	13	US-10-027-632-264348	Sequence 264348,
c 44	243.8	10.1	301	10	US-09-860-670-183	Sequence 183, App
45	243.8	10.1	1843	13	US-10-027-632-100497	Sequence 100497,

ALIGNMENTS

RESULT 1

US-09-899-532-3
; Sequence 3, Application US/09899532
; Patent No. US20020048791A1
; GENERAL INFORMATION:
; APPLICANT: Bloomquist, Brian T.
; APPLICANT: Zhelnin, Leonid
; TITLE OF INVENTION: Human Neuropeptide Y-Like G
; FILE OF INVENTION: Protein-Coupled Receptor
; FILE REFERENCE: 02973.00040
; CURRENT APPLICATION NUMBER: US/09/899,532
; CURRENT FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: US 60/216,523
; PRIOR FILING DATE: 2000-07-06
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1710
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-899-532-3

Query Match	69.1%	Score 1668.4;	DB 9;	Length 1710;
Best Local Similarity	99.9%;	Pred. No. 0;		
Matches 1669;	Conservative	0;	Mismatches	1;
Indels	0;	Gaps	0;	
QY	1	GCCAGAGCGCCAGGACCTTACGCTGGCGCTCCAGACCCAGACCGTGGCGGCGCTCG	60	
Db	41	GCCAGAGCGCCAGGACCTTACGCTGGCGCTCCAGACCCAGACCGTGGCGGCGCTCG	100	
QY	61	CCCTAGGGAAGACGAGGAGAACTTATTGACCGGGAACATTTTTCCTGCTAG	120	
Db	101	CCCTAGGGAAGACGAGGAGAACTTATTGACCGGGAACATTTTTCCTGCTAG	160	
QY	121	ATCCAGTCTCCAGTCTTTCGCTTCCGCTCTTTTCGCTGCTGCTGCTGCTGCTGCTG	180	
Db	161	ATCCAGTCTCCAGTCTTTCGCTTCCGCTCTTTTCGCTGCTGCTGCTGCTGCTGCTG	220	
QY	181	CTCTCTTTTCCGAACTCCCGGGTGCAGCCTAGACCTTCCCGCGCGCTGACTCCAG	240	

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Db 221 CTCTCTCTCCCGAACCTCCCGGGGTGACGCTTAGAGCCCTCCCGCGCGCTGACTCCAG 280
Qy 241 AGTAGAGGAGGAGCGCGCTCCGGCTGGTCCCGGAAGCCCTGCTGCCCGGAGATG 300
Db 281 AGTAGAGGAGGAGCGCGCTCCGGCTGGTCCCGGAAGCCCTGCTGCCCGGAGATG 340
Qy 301 CGGATGGCCAGCAGTAGCGGGGGTGGCCCGCGCTCCCGGAGCGCAGCAATGCGAG 360
Db 341 CGGATGGCCAGCAGTAGCGGGGGTGGCCCGCGCTCCCGGAGCGCAGCAATGCGAG 400
Qy 361 CGCTTAACATTACCCCGAGAGTCTCTCGGCTGCTGCGGAGCACAACCTGACGCGG 420
Db 401 CGCTTAACATTACCCCGAGAGTCTCTCGGCTGCTGCGGAGCACAACCTGACGCGG 460
Qy 421 AGCAGTTCACTGCTGACCGGCTCGGACCGCTGCTTACACCCAGAGCTGCCGGGAC 480
Db 461 AGCAGTTCACTGCTGACCGGCTCGGACCGCTGCTTACACCCAGAGCTGCCGGGAC 520
Qy 481 GGGCCAAGCTGGCCCTCGTGCTCACCGGCGTGTCTATCTTCGCCCTGGGCGCTCTTGGCA 540
Db 521 GGGCCAAGCTGGCCCTCGTGCTCACCGGCGTGTCTATCTTCGCCCTGGGCGCTCTTGGCA 580
Qy 541 ATGCTCTGCTGCTTACGTTGTAACCGGAGCAAGCCGATGCGCACCGTCAACAACAT 600
Db 581 ATGCTCTGCTGCTTACGTTGTAACCGGAGCAAGCCGATGCGCACCGTCAACAACAT 640
Qy 601 TTATCTGCTCTTGGCGCTCAGTGACCTGCTCATCACCTTCTCTGCTATCCCGTCACCA 660
Db 641 TTATCTGCTCTTGGCGCTCAGTGACCTGCTCATCACCTTCTCTGCTATCCCGTCACCA 700
Qy 661 TGCTCCAGAACATTTCCGCAACTGCTGGGGGTGCTTTCATTTGCAAGATGGTGCCAT 720
Db 701 TGCTCCAGAACATTTCCGCAACTGCTGGGGGTGCTTTCATTTGCAAGATGGTGCCAT 760
Qy 721 TTGTCAGGCTACCGCTGTGTGACAGAAATCTCTATGACCTGCAATGCTGTGGAAA 780
Db 761 TTGTCAGGCTACCGCTGTGTGACAGAAATCTCTATGACCTGCAATGCTGTGGAAA 820
Qy 781 GGCACAGGAGCTGTGCAATCTTTTAAATGAAGTGGCAATACACCAACCGAAGGCTT 840
Db 821 GGCACAGGAGCTGTGCAATCTTTTAAATGAAGTGGCAATACACCAACCGAAGGCTT 880
Qy 841 TCACATGCTAGTGTGTGCTGGCTGGCAGTCACTGATGATCACCATGCTGGCAG 900
Db 881 TCACATGCTAGTGTGTGCTGGCTGGCAGTCACTGATGATCACCATGCTGGCAG 940
Qy 901 TGCACAACTTGAGATCAATATGACTTCGTATATGAAAGGAACACATCTGCTGTAG 960
Db 941 TGCACAACTTGAGATCAATATGACTTCGTATATGAAAGGAACACATCTGCTGTAG 1000
Qy 961 AAGAGTGGACCAAGCCCTGTGCACAGAGATCTACACCACTTCATCTTGTGATCTCT 1020
Db 1001 AAGAGTGGACCAAGCCCTGTGCACAGAGATCTACACCACTTCATCTTGTGATCTCT 1060
Qy 1021 TCTCTGCTCTTATGTTGATGCTTATCTGTGACAGTAAATGTTGTTAGACTTTGGA 1080
Db 1061 TCTCTGCTCTTATGTTGATGCTTATCTGTGACAGTAAATGTTGTTAGACTTTGGA 1120
Qy 1081 TAAAGAAAAGAGTTGGGATGTTTCACTGCTCGAATCTTCAATGAAAGAAATGTCGA 1140
Db 1121 TAAAGAAAAGAGTTGGGATGTTTCACTGCTCGAATCTTCAATGAAAGAAATGTCGA 1180
Qy 1141 AAATAGCCAGGAAGAAACAGAGCTGTCAATATGATGTTGAGTGGTCTCTTTTG 1200
Db 1181 AAATAGCCAGGAAGAAACAGAGCTGTCAATATGATGTTGAGTGGTCTCTTTTG 1240
Qy 1201 CTGTGTGCTGGGACCAATTCATGTTGTCATATGATGATGATGATGATGATGATG 1260
Db 1241 CTGTGTGCTGGGACCAATTCATGTTGTCATATGATGATGATGATGATGATGATG 1300
Qy 1261 AGGAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1320
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Db 1301 AGGAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1360
Qy 1321 CCAACTCCATCTTAATCCCAATTCCTATGATGATGATGATGATGATGATGATGAT 1380
Db 1361 CCAACTCCATCTTAATCCCAATTCCTATGATGATGATGATGATGATGATGATGAT 1420
Qy 1381 TTTTGTCTGCAAGTTGTTATTGTCATAGTAAATAAACCTTCTCCAGCACAAAGGCA 1440
Db 1421 TTTTGTCTGCAAGTTGTTATTGTCATAGTAAATAAACCTTCTCCAGCACAAAGGCA 1480
Qy 1441 GAAATTCAGGAATTAACAATGATGGGAGAAAGCAAAAGTCTTCCCTCAGAGAAATCCAG 1500
Db 1481 GAAATTCAGGAATTAACAATGATGGGAGAAAGCAAAAGTCTTCCCTCAGAGAAATCCAG 1540
Qy 1501 TGGAGGAAACCAAGGAGAGCAATTCAGTGATGGCAACATTTGATGATGATGATGATG 1560
Db 1541 TGGAGGAAACCAAGGAGAGCAATTCAGTGATGGCAACATTTGATGATGATGATGATG 1600
Qy 1561 AGACAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1620
Db 1601 AGACAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1660
Qy 1621 AGAATTCCTCTTTAGACAGTGGGCAATTAATTAACAATATCTTCAATAT 1670
Db 1661 AGAATTCCTCTTTAGACAGTGGGCAATTAATTAACAATATCTTCAATAT 1710
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RESULT 2

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US-10-080-263C-1
; Sequence 1, Application US/10080263C
; Publication No. US20030143670A1
; GENERAL INFORMATION:
; APPLICANT: Bonini, James A.
; APPLICANT: Huang, Ling-Yan
; APPLICANT: Wilson, Amy
; TITLE OF INVENTION: DNA ENCODING SNORF44 RECEPTOR
; FILE REFERENCE: 1795/59370-A/JPW/ADM/ANX
; CURRENT APPLICATION NUMBER: US/10/080,263C
; CURRENT FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1495
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-080-263C-1
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Query Match 61.9%; Score 1495; DB 12; Length 1495;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1495; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 CTCTCTTTCCCGAACCTCCCGGGTGCAGCTAGAGCCCTCCCGCGGCTGACTCCAG 60
Qy 241 AGTAGAGGAGGAGGCGGCGCTCCGCGCTGGTCCCGGAAGCCCTGCTGCCCGCAGATG 300
Db 61 AGTAGAGGAGGAGGCGGCGCTCCGCGCTGGTCCCGGAAGCCCTGCTGCCCGCAGATG 120
Qy 301 CGGATGGCCAGCAGTAGCGGCGGTGCGCGCTGCGCGGAGCGGCAACAGCAATGCAAG 360
Db 121 CGGATGGCCAGCAGTAGCGGCGGTGCGCGCTGCGCGGAGCGGCAACAGCAATGCAAG 180
Qy 361 CGCTTAACATTACCCCGAGAGTCTCTCGGCTGCTCGGGAACCAACACTGACGCGGG 420
Db 181 CGCTTAACATTACCCCGAGAGTCTCTCGGCTGCTCGGGAACCAACACTGACGCGGG 240
Qy 421 AGCAGTTCACTGCTGACCGGCTGCGACCGCTGCTTACACCCAGAGCTGCCGGGAC 480
Db 241 AGCAGTTCACTGCTGACCGGCTGCGACCGCTGCTTACACCCAGAGCTGCCGGGAC 300
Qy 481 GGGCCAAGCTGGCCCTCTGCTGCTACCGGCGTGTCTATCTTCGCCCTGGGCGCTCTTGGCA 540
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Db 301 CGGCAAGCTGGCCCTCTGTGCTCACGGGGTGGCTCACTTCGGCCCTGGCGCTCTTTGGCA 360
Qy 541 ATGCTCTGGTGTCTACGTGGTGACCCGACGAGGCGCATGGCGACCGCTCAACCAACTCT 600
Db 361 ATGCTCTGGTGTCTACGTGGTGACCCGACGAGGCGCATGGCGACCGCTCAACCAACTCT 420
Qy 601 TTAATCTGCTCCTTGGCGCTCAGTGACCTGCTCATCACCTTCTTCTGCAATCCCGTCACCA 660
Db 421 TTAATCTGCTCCTTGGCGCTCAGTGACCTGCTCATCACCTTCTTCTGCAATCCCGTCACCA 480
Qy 661 TGCTCCAGAAATCTCCACAACTGGCTGGGGGTGCTTTCATTTGCAAGATGTGCCAT 720
Db 481 TGCTCCAGAAATCTCCACAACTGGCTGGGGGTGCTTTCATTTGCAAGATGTGCCAT 540
Qy 721 TTGTCCAGTCTACCGCTCTGTGACAGAAATCCTCACTATGACCTGCAATGCTGTGGAAA 780
Db 541 TTGTCCAGTCTACCGCTCTGTGACAGAAATCCTCACTATGACCTGCAATGCTGTGGAAA 600
Qy 781 GGCACACGGGACTTGTGATCCTTTTAAATGAATGGAATGGAATACCAACCGAAGGGCTT 840
Db 601 GGCACACGGGACTTGTGATCCTTTTAAATGAATGGAATGGAATACCAACCGAAGGGCTT 660
Qy 841 TCAGATCTAGGTGTGCTGGCTGGCTGGCGAGTCATGCTAGGATCACCCATGTGGCAG 900
Db 661 TCAGATCTAGGTGTGCTGGCTGGCTGGCGAGTCATGCTAGGATCACCCATGTGGCAG 720
Qy 901 TGCACAACTTGAGATCAATATGACTTCCATATGAAAAGGAACACATCTGCTCTTAG 960
Db 721 TGCACAACTTGAGATCAATATGACTTCCATATGAAAAGGAACACATCTGCTCTTAG 780
Qy 961 AAGAGTGAACGACGCTGTGACACGAGAAGTCTACACACCTTCATCCTTGTCTCCTCT 1020
Db 781 AAGAGTGAACGACGCTGTGACACGAGAAGTCTACACACCTTCATCCTTGTCTCCTCT 840
Qy 1021 TCCTCTCCCTTATGATGATGCTTATCTGTACAGTAAATGCTTATGAACTTTGGA 1080
Db 841 TCCCTCCCTTATGATGATGCTTATCTGTACAGTAAATGCTTATGAACTTTGGA 900
Qy 1081 TAAAGAAAAGAGTGGGGATGGTTCAGTGTCTCGAACTATTATGAGAAAAGAAATGTCCA 1140
Db 901 TAAAGAAAAGAGTGGGGATGGTTCAGTGTCTCGAACTATTATGAGAAAAGAAATGTCCA 960
Qy 1141 AAATAGCCAGAAAGAAAGCTGTCTATATGATGGTGACAGTGGTGGCTCTCTTTG 1200
Db 961 AAATAGCCAGAAAGAAAGCTGTCTATATGATGGTGACAGTGGTGGCTCTCTTTG 1020
Qy 1201 CTGTGTGTGGGCACCATTCATGATGTGCCATGATGATGAATACAGTAAATTTGAAA 1260
Db 1021 CTGTGTGTGGGCACCATTCATGATGTGCCATGATGATGAATACAGTAAATTTGAAA 1080
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Db 1081 AGGAATATGATGATGATGATCAATCAAGATGATTTTGTCTATGCTGCAAAATTTGGAATTT 1140
Qy 1321 CCAACTCCATCTGTAATCCCATGCTATGCAATTTATGAATGAACCTTCAAAAAAATG 1380
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Db 1201 TTTTCTGTGCAATTTGTTATGTCATAGTAAATATAAACCTTCTCTCAGCACAAAGGCATG 1260
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Qy 1501 TGGAGGAAACCAAAGAGAGCAATTCAGTGTGGCAACATTAAGTCAAAATGTGTGAAC 1560
Db 1321 TGGAGGAAACCAAAGAGAGCAATTCAGTGTGGCAACATTAAGTCAAAATGTGTGAAC 1380
Qy 1561 AGACAGAGAGAGAGAAAGCTCAACGACATCTTCTCTTTAGGCTGAACTGGGCTG 1620
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Qy 1621 AGAATTCCTTTAGACAGTGGGCATTAATTAACAATATCTTCAATAATTAATG 1675
Db 1441 AGAATTCCTTTAGACAGTGGGCATTAATTAACAATATCTTCAATTAATG 1495
RESULT 3
US-09-826-508-21
; Sequence 21, Application US/09826508
; Patent No. US20010025099A1
; GENERAL INFORMATION:
; APPLICANT: Nabil Elshourbagy
; APPLICANT: Lisa Vawter
; TITLE OF INVENTION: G Protein-Coupled Receptor Polypeptides
; TITLE OF INVENTION: and Polynucleotides
; FILE REFERENCE: GP-70744USB
; CURRENT APPLICATION NUMBER: US/09/826,508
; CURRENT FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 1296
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
US-09-826-508-21
Query Match 53.7%; Score 1296; DB 9; Length 1296;
Best Local Similarity 100.0%; Pred. No. 1.3e-285;
Matches 1296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 354 ATGCAGCGCTTAACATTAACCCCGAGCAGTTCTCTCGGTGCTGCGGACCAACCTG 413
Db 1 ATGCAGCGCTTAACATTAACCCCGAGCAGTTCTCTCGGTGCTGCGGACCAACCTG 60
Qy 414 ACGGGGAGCAGTTCACTCGCTCTGTCGCGTGGAGCGCTCGTCTACACCCAGAGCTG 473
Db 61 ACGGGGAGCAGTTCACTCGCTCTGTCGCGTGGAGCGCTCGTCTACACCCAGAGCTG 120
Qy 474 CCGGACGCGCAAGCTCGTCTCACCGCGCTGCTCATCTTGGCCCTGGCGCTC 533
Db 121 CCGGACGCGCAAGCTCGTCTCACCGCGCTGCTCATCTTGGCCCTGGCGCTC 180
Qy 534 TTTGGCAATGCTCTGGTGTCTACGTGTGACCCGAGCAAGGCATGCGCACCGTACC 593
Db 181 TTTGGCAATGCTCTGGTGTCTACGTGTGACCCGAGCAAGGCATGCGCACCGTACC 240
Qy 594 AACATCTTTATCTGCTCTTGGCGCTCAGTGACCTGCTCATCCTTCTTCTGCAATCCC 653
Db 241 AACATCTTTATCTGCTCTTGGCGCTCAGTGACCTGCTCATCCTTCTTCTGCAATCCC 300
Qy 654 GTCACCATGCTCCAGAAACATTTCCGACAACTGGCTGGGGGTGCTTTTCATTTGCAAGATG 713
Db 301 GTCACCATGCTCCAGAAACATTTCCGACAACTGGCTGGGGGTGCTTTTCATTTGCAAGATG 360
Qy 714 GTGCCATTTGTCAGTCTACCGCTGTTGTGACAGAAATCTCACTATGACCTGCAATGCT 773
Db 361 GTGCCATTTGTCAGTCTACCGCTGTTGTGACAGAAATCTCTCACTATGACCTGCAATGCT 420
Qy 774 GTGGAAGGCAACCGAGGACCTTGTGCATCTCTTTAAATGAAGTGGCAATACCAACCGA 833
Db 421 GTGGAAGGCAACCGAGGACCTTGTGCATCTCTTTAAATGAAGTGGCAATACCAACCGA 480
Qy 834 AGGCTTTTCAAAATGCTAGTGTGCTGCTGGTGGCAGTCACTCGTAGGATCAACCATG 893
Db 481 AGGCTTTTCAAAATGCTAGTGTGCTGCTGGTGGCAGTCACTCGTAGGATCAACCATG 540
Qy 894 TGGCACTGTGCAACCACTTGGATCAAAATATGACTTCTATATGAAAAAGGAACAATCTGC 953
Db 541 TGGCACTGTGCAACCACTTGGATCAAAATATGACTTCTATATGAAAAAGGAACAATCTGC 600
Qy 954 TGCTTAGAAGTGGACGAGCCCTGTGCAACGAGAGATCTACACCACTTCACTCTGTGTC 1013
Db 601 TGCTTAGAAGTGGACGAGCCCTGTGCAACGAGAGATCTACACCACTTCACTCTGTGTC 660


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Db 1081 AGGCATGAAATTCAGGAATTACAAATGATGCGGAAGAAAGCAAAAGTTTTCCTCAGAGAG 1140
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Db 1141 AATCCAGTGGAGGAAACCAAGGAGGAAGCAATTCAGTGTATGATGCAACATTTGAAGTCAAAATTG 1200
Qy 1554 TGTGAACAGACAGAGGAGAAAGAAAGCTCAAAACGACATCTTCTTTAGTCTGAA 1613
Db 1201 TGTGAACAGACAGAGGAGAAAGAAAGCTCAAAACGACATCTTCTTTAGTCTGAA 1260
Qy 1614 CTGCTGAGAAATTCCTTTAGACAGTGGGCAATTA 1649
Db 1261 CTGCTGAGAAATTCCTTTAGACAGTGGGCAATTA 1296

RESULT 5
US-09-990-940-5
; Sequence 5, Application US/09990940
; Publication No. US20030027252A1
; GENERAL INFORMATION:
; APPLICANT: Tian, Hui
; APPLICANT: Zhao, Jiaqiang
; APPLICANT: Chen, Jin-Long
; APPLICANT: Cuclier, Gene
; APPLICANT: An, Songzhu
; APPLICANT: Dai, Kang
; APPLICANT: Gupte, Jamila S.
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: No. US20030027252A1el Receptors
; FILE REFERENCE: 018781-007410US
; CURRENT APPLICATION NUMBER: US/09/990,940
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/252,841
; PRIOR FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: US 60/257,636
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 60/261,377
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 60/279,554
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 60/280,696
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 5
; LENGTH: 1296
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1296)
; OTHER INFORMATION: human G-protein coupled receptor (GPCR) TGR346
US-09-990-940-5

Query Match 53.7%; Score 1296; DB 11; Length 1296;
Best Local Similarity 100.0%; Pred. No. 1.3e-285;
Matches 1296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 354 ATGCAGGCGCTTAACATTACCCGAGCAGTTCCTCGGCTGCTCGGAGCCACAACTG 413
Db 1 ATGCAGGCGCTTAACATTACCCGAGCAGTTCCTCGGCTGCTCGGAGCCACAACTG 60
Qy 414 ACGCGGAGCAGTTTCATCGCTGTACCGGCTGCGACGCGCTGTACACCCCGAGCTG 473
Db 61 ACGCGGAGCAGTTTCATCGCTGTACCGGCTGCGACGCGCTGTACACCCCGAGCTG 120
Qy 474 CCGGAGCGGCCAAGCTGCGCTGTACCGGCGTGTCTATCTGCGCTGCGGCTC 533
Db 121 CCGGAGCGGCCAAGCTGCGCTGTACCGGCGTGTCTATCTGCGCTGCGGCTC 180
Qy 534 TTTGGCAATGCTCTGGTGTCTACGTGTGACCGCAGCAGGCCATGGCACCTGACC 593
Db 181 TTTGGCAATGCTCTGGTGTCTACGTGTGACCGCAGCAGGCCATGGCACCTGACC 240
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Qy 594 AACATCTTTATCTGCTCTTTGGCGCTCAGTGACCTGCTCATCACTTCTTCTGCAATCCC 653
Db 241 AACATCTTTATCTGCTCTTTGGCGCTCAGTGACCTGCTCATCACTTCTTCTGCAATCCC 300
Qy 654 GTACCACTGCTCAGAACATTTCCGACAACTGCTGGGGGTGCTTTCATTTGCAAGATG 713
Db 301 GTACCACTGCTCAGAACATTTCCGACAACTGCTGGGGGTGCTTTCATTTGCAAGATG 360
Qy 714 GTGCAATTTCTCAGTCTACCGCTGTGTGACAGAAATCTCTCATATGACCTGCAATGCT 773
Db 361 GTGCAATTTCTCAGTCTACCGCTGTGTGACAGAAATCTCTCATATGACCTGCAATGCT 420
Qy 774 GTGGAAGGCAACAGGAGCTTTGTGCATCTCTTTAAATGAAGTGGCAATACACCAACCGA 833
Db 421 GTGGAAGGCAACAGGAGCTTTGTGCATCTCTTTAAATGAAGTGGCAATACACCAACCGA 480
Qy 834 AGGCTTTTCAATGCTAGTGTGGTCTGCTGGTGGCAGTCACTGAGATCACCCATG 893
Db 481 AGGCTTTTCAATGCTAGTGTGGTCTGCTGGTGGCAGTCACTGAGATCACCCATG 540
Qy 894 TGGCAGCTGCAACAACTTGAGATCAAAATATGACTTCTATATGAAAAAGGAACACATCTGC 953
Db 541 TGGCAGCTGCAACAACTTGAGATCAAAATATGACTTCTATATGAAAAAGGAACACATCTGC 600
Qy 954 TGTTAGAAGTGGACCAAGCTGTGCAACAGAGATCTACACCACTTCACTCTTGTCT 1013
Db 601 TGTTAGAAGTGGACCAAGCTGTGCAACAGAGATCTACACCACTTCACTCTTGTCT 660
Qy 1014 ATCTCTCTCTCTCTCTCTTATGATGCTTATCTGTACAGTAAATTTGGTTATGAA 1073
Db 661 ATCTCTCTCTCTCTCTCTTATGATGCTTATCTGTACAGTAAATTTGGTTATGAA 720
Qy 1074 CTTTGGATAAAGAAAAGAGTTGGGATGGTTTCAGTGTCTCGAACTATTCATGGAAGAA 1133
Db 721 CTTTGGATAAAGAAAAGAGTTGGGATGGTTTCAGTGTCTCGAACTATTCATGGAAGAA 780
Qy 1134 ATGTCCAAAATAGCCAGGAAGAAACGAGCTGCTCATATGATGGTGACAGTGGTGGCT 1193
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Qy 1194 CTCTTTGCTGTGCTGGCAGCATTCCATGTTGCTCATATGATGATGAATACAGTAAT 1253
Db 841 CTCTTTGCTGTGCTGGCAGCATTCCATGTTGCTCATATGATGATGAATACAGTAAT 900
Qy 1254 TTTGAAAAGGAATATGATGATGTCACAATCAAGATGATTTTGTCTATCGTCAAAATATT 1313
Db 901 TTTGAAAAGGAATATGATGATGTCACAATCAAGATGATTTTGTCTATCGTCAAAATATT 960
Qy 1314 GGATTTTCCAACTCCATCTGTAATCCCATTTGCTATGCAATTTATGAATGAAAATCTCAA 1373
Db 961 GGATTTTCCAACTCCATCTGTAATCCCATTTGCTATGCAATTTATGAATGAAAATCTCAA 1020
Qy 1374 AAAATGCTTTGCTGCGAGTTTGTATTGCAATAGTAAATAAAACCTTCTCTCCAGCAAA 1433
Db 1021 AAAATGCTTTGCTGCGAGTTTGTATTGCAATAGTAAATAAAACCTTCTCTCCAGCAAA 1080
Qy 1434 AGGCATGGAATTCAGGAATTTACAAATGATGCGGAAGAAAGCAAAAGTTTTCCTCAGAGAG 1493
Db 1081 AGGCATGGAATTCAGGAATTTACAAATGATGCGGAAGAAAGCAAAAGTTTTCCTCAGAGAG 1140
Qy 1494 AATCCAGTGGAGAAACCAAGGAGAGCAATTCAGTGTATGATGCAACATTTGAAGTCAAAATTG 1553
Db 1141 AATCCAGTGGAGAAACCAAGGAGAGCAATTCAGTGTATGATGCAACATTTGAAGTCAAAATTG 1200
Qy 1554 TGTGAACAGACAGAGGAGAAAGAAAGCTCAAAACGACATCTTGTCTCTTTAGTCTGAA 1613
Db 1201 TGTGAACAGACAGAGGAGAAAGAAAGCTCAAAACGACATCTTGTCTCTTTAGTCTGAA 1260
Qy 1614 CTGCTGAGAAATTCCTTTAGACAGTGGGCAATTA 1649
Db 1261 CTGCTGAGAAATTCCTTTAGACAGTGGGCAATTA 1296
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RESULT 6
US-10-272-983-37
; Sequence 37, Application US/10272983
; Publication No. US20030148450A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Dang, Huong T.
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
; FILE REFERENCE: AREN0050
; CURRENT APPLICATION NUMBER: US/10/272,983
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: US/09/417,044
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 60/109,213
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,851
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/123,946
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,949
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/136,436
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,437
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,439
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,567
; PRIOR FILING DATE: 1999-05-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 37
; LENGTH: 1296
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-272-983-37

Query Match      53.6%; Score 1294.4; DB 12; Length 1296;
Best Local Similarity 99.9%; Pred. No. 2.9e-285;
Matches 1295; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 354 ATCCAGGCGCTTAACATTAACCCCGGAGCAGTCTCTCGGCTGCTGGGACCAACACCTG 413
DB 1 ATCCAGGCGCTTAACATTAACCCCGGAGCAGTCTCTCGGCTGCTGGGACCAACACCTG 60

QY 414 ACGCGGGAGCAGTTTCATCGCTGTGTACCGGCTGCGACCGCTGCTACACCCCGCAGAGCTG 473
DB 61 ACGCGGGAGCAGTTTCATCGCTGTGTACCGGCTGCGACCGCTGCTACACCCCGCAGAGCTG 120

QY 474 CCGGGACGCGCAAGTGCCTCGTGTCTACCGGCTGCTCATCTTCGCCCTGGCGCTC 533
DB 121 CCGGGACGCGCAAGTGCCTCGTGTCTACCGGCTGCTCATCTTCGCCCTGGCGCTC 180

QY 534 TTGTGGCAATGCTGTGTGTCTACGTGTGTGACCGGACGAGCCATGGCGACCGTCAAC 593
DB 181 TTGTGGCAATGCTGTGTGTCTACGTGTGTGACCGGACGAGCCATGGCGACCGTCAAC 240

QY 594 AACATCTTTATCTGCTTCTGGGCTCAGTGACCTGCTCATCACCTTCTTCTGCAATGCC 653
DB 241 AACATCTTTATCTGCTTCTTGGGCTCAGTGACCTGCTCATCACCTTCTTCTGCAATGCC 300

QY 654 GTCAACATGCTCCAGAACATTTCCGACAACTGGCTGGGGGTGCTTTCAATTTGCAAGATG 713
DB 301 GTCAACATGCTCCAGAACATTTCCGACAACTGGCTGGGGGTGCTTTCAATTTGCAAGATG 360

QY 714 GTGCCATTTTCCAGTCTACCGCTGTGTGACAGAAATCCTCACATGACCTGCAATGCT 773
DB 714 GTGCCATTTTCCAGTCTACCGCTGTGTGACAGAAATCCTCACATGACCTGCAATGCT 773
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RESULT 7

US-10-393-807-37

; Sequence 37, Application US/10393807

; Publication No. US20030175891A1

; GENERAL INFORMATION:

; APPLICANT: Chen, Ruoping

; APPLICANT: Dang, Huong T.

; APPLICANT: Liaw, Chen W.

; APPLICANT: Lin, I-Lin

; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors

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DB 361 GTGCCATTTTCTCCAGTCTACCGCTGTGTGTGACAGAAATGCTCACTATGACCTGCAATGCT 420
QY 774 GTGHAAGGACACCGGACTTGTGCACTCTTTTAAATGAAGTGGCAATACACCAACCGA 833
DB 421 GTGHAAGGACACCGGACTTGTGCACTCTTTTAAATGAAGTGGCAATACACCAACCGA 480
QY 834 AGGGCTTTTCAAAATCTAGGTGTGTGTGCTGGTGGGAGTCACTGTAAGTACCCCATG 893
DB 481 AGGGCTTTTCAAAATCTAGGTGTGTGTGCTGGTGGGAGTCACTGTAAGTACCCCATG 540
QY 894 TGGCACGTGCAACAACTTTGAGATCAAAATATGACTTCTTATATGAAAGGAAACACATCTGC 953
DB 541 TGGCACGTGCAACAACTTTGAGATCAAAATATGACTTCTTATATGAAAGGAAACACATCTGC 600
QY 954 TGCCTTAGAGAGTGGACGACCCCTGTGCAACAGAAATCTACACACCTTCACTCTGTC 1013
DB 601 TGCCTTAGAGAGTGGACGACCCCTGTGCAACAGAAATCTACACACCTTCACTCTGTC 660
QY 1014 ATCCCTTCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1073
DB 661 ATCCCTTCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
QY 1074 CTTTGGATATAAGAAAGAGTTGGGATGTTTGGGATGTTTGGGATGTTTGGGATGTTTGGGATGTT 1133
DB 721 CTTTGGATATAAGAAAGAGTTGGGATGTTTGGGATGTTTGGGATGTTTGGGATGTTTGGGATGTT 780
QY 1134 ATGTCCAAATAGCCAGGAGAAAGAACAGCTGTCTATATGATGCTGACAGTGTGCTGCT 1193
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DB 841 CTCTTTGCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
QY 1254 TTTGAAAAGGAATATGATGATGTCTCAATCAAGATGATTTTGTCTATGCTGCAATTTT 1313
DB 901 TTTGAAAAGGAATATGATGATGTCTCAATCAAGATGATTTTGTCTATGCTGCAATTTT 960
QY 1314 GGATTTTCCAACTCCATCTGTAATCCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1373
DB 961 GGATTTTCCAACTCCATCTGTAATCCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
QY 1374 AAAAATGTTTGTCTGCACTGTTTGTATTGCAATGATAAATAAAACCTTCTCTCCAGCAAA 1433
DB 1021 AAAAATGTTTGTCTGCACTGTTTGTATTGCAATGATAAATAAAACCTTCTCTCCAGCAAA 1080
QY 1434 AGGATGAAATTCAGGAATTAACAATGATGCGGAAGAAAGCAAAAGTTTTCCTCTCAGAGAG 1493
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QY 1494 AATCCAGTGGAGGAAACCAAGAGGAGAGCAATTCAGTGTGATGCAATTTGAAGTCAAAATG 1553
DB 1141 AATCCAGTGGAGGAAACCAAGAGGAGAGCAATTCAGTGTGATGCAATTTGAAGTCAAAATG 1200
QY 1554 TGTGAACAGACAGAGGAGAGAAAGAAAGCTCAAAAGCAATCTTGTCTCTTTAGTCTCTGAA 1613
DB 1201 TGTGAACAGACAGAGGAGAGAAAGAAAGCTCAAAAGCAATCTTGTCTCTTTAGTCTCTGAA 1260
QY 1614 CTGGCTGAGAAATTCCTTTTAGACAGTGGGCATTA 1649
DB 1261 CTGGCTGAGAAATTCCTTTTAGACAGTGGGCATTA 1296
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FILE REFERENCE: AREN0050
; CURRENT APPLICATION NUMBER: US/10/393,807
; CURRENT FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: US/09/417,044
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 60/109,213
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,851
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/123,946
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,949
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/136,436
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,437
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,439
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,567
; PRIOR FILING DATE: 1999-05-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 37
; LENGTH: 1296
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-393-807-37

Query Match 53.6%; Score 1294.4; DB 12; Length 1296;
Best Local Similarity 99.9%; Pred. No. 2.9e-285;
Matches 1295; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 354 ATGCAGGGCGTTACATTACCCCGAGAGTCTCTCGGCTGTCGGGAGACACACCTG 413
DB 1 ATGCAGGGCGTTAACTTACCCCGAGAGTCTCTCGGCTGTCGGGAGACACACCTG 60

QY 414 ACGGGGAGAGTTCATCGCTCTGTACCGCTGCGACCGCTGCTACACCCGAGAGTG 473
DB 61 ACGGGGAGAGTTCATCGCTCTGTACCGCTGCGACCGCTGCTACACCCGAGAGTG 120

QY 474 CCGGAGCGCCAAAGCTGGCCCTCGTGTCTACCGGCTGCTCATCTTCGCCCTGCGGCTC 533
DB 121 CCGGAGCGCCAAAGCTGGCCCTCGTGTCTACCGGCTGCTCATCTTCGCCCTGCGGCTC 180

QY 534 TTTGGCAATGCTCTGGTGTCTTACGCTGTGAGCCGACAGGCCATCGCACCGTCAAC 593
DB 181 TTTGGCAATGCTCTGGTGTCTTACGCTGTGAGCCGACAGGCCATCGCACCGTCAAC 240

QY 594 AACATCTTTATCTGCTCTCGGCTCAGTGACCTGCTCATCACTTCTTCTGCAATCCC 653
DB 241 AACATCTTTATCTGCTCTCGGCTCAGTGACCTGCTCATCACTTCTTCTGCAATCCC 300

QY 654 GTCACCATGCTCCAGAACATTCGACAACTGGCTGGGGGGTCTTTCATTTCGAAGATG 713
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QY 714 GTGGCAATTTGTCAGTCTACCGCTTGTGACAGAAATCCCTCACTATACCTGCAATGCT 773
DB 361 GTGGCAATTTGTCAGTCTACCGCTTGTGACAGAAATCCCTCACTATACCTGCAATGCT 420

QY 774 GTGGAAAGGCACCGAGGACTTGTGTCATCTTTTAAATGAAGTGGCAATACACCAACCGA 833
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QY 834 AGGGCTTTTCAATGCTAGGTGTGCTCTGGCTGGTGGCAGTCACTGCTAGGATCAACCATG 893
DB 481 AGGGCTTTTCAATGCTAGGTGTGCTCTGGCTGGTGGCAGTCACTGCTAGGATCAACCATG 540

QY 894 TGGCAGCTGCAACACTTGTAGATCAAAATATGACTTCTCTATATGAAGAAAGCAATCTGC 953

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DB 601 TGCTTAGAGAGTGGACCCGCTGTGSCACAGAGATCTACACCACTTCATCTCTGTC 660
QY 1014 ATCTCTTCT 1073
DB 661 ATCTCTTCT 720
QY 1074 CTTTGGATAAAGAAAGAGTTGGGGATGGTTCCATGTTTCCATATGATGATTGAATACAGTAAT 1133
DB 721 CTTTGGATAAAGAAAGAGTTGGGGATGGTTCCATGTTTCCATATGATGATTGAATACAGTAAT 780
QY 1134 ATGTCCAAATATGCCAGGAGAGAAACGAGCTGTCATTAATGATGGTGACAGTGGTGGCT 1193
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QY 1194 CTCTTTGCTGTGCTGGGACCACTTCCATGTTTCCATATGATGATTGAATACAGTAAT 1253
DB 841 CTCTTTGCTGTGCTGGGACCACTTCCATGTTTCCATATGATGATTGAATACAGTAAT 900
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DB 901 TTTGAAAAGGAATATGATGATGTGCACAAATCAAGATGATTTTGGCTATCGTCAAAATATT 960
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DB 961 GGATTTTCCAACTCCATCTGTAATCCCATGTTCTATGCAATTTATGAATGAAACTTCAAA 1020
QY 1374 AAAAATGTTTGTGTCAGTTTGTATTGTCATAGTAAATAAAACCTTCTCTCCAGCAAA 1433
DB 1021 AAAAATGTTTGTGTCAGTTTGTATTGTCATAGTAAATAAAACCTTCTCTCCAGCAAA 1080
QY 1434 AGGCATGGAATTCAGGAATTCAGTAATGATGCGGAGAAAGCAAGTTTTCCTCAGAGAG 1493
DB 1081 AGGCATGGAATTCAGGAATTCAGTAATGATGCGGAGAAAGCAAGTTTTCCTCAGAGAG 1140
QY 1494 AATCCAGTGAGGAAACCAAGGAGAGAGCATTCAGTGATGCGAACATTTGAAGTCAAAATTG 1553
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QY 1614 CTGGCTCAGAAATCTCTCTTTAGACAGTGGGCAATTA 1649
DB 1261 CTGGCTCAGAAATCTCTCTTTAGACAGTGGGCAATTA 1296

RESULT 8
US-10-225-567A-509
; Sequence 509, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Glena C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTOR
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 509
; LENGTH: 1368
; TYPE: DNA
; ORGANISM: Homo sapiens

US-10-225-567A-509

Query Match					
44.7%; Score 1078.4; DB 14; Length 1368;					
Best Local Similarity 91.3%; Refid No. 6.2e-236;					
Matches 1213; Conservative 0; Mismatches 1; Indels 114; Gaps 2;					
Qy	322	CGCGTGGCCCGCGCTCCCGGAGGGGCACAGCAATATGACGGCGCTTAACAATTACCACCGGAGC	381		
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Qy	382	AGTTCTCTGGGTGCTGGGAGACACAACTGAACGGGAGAGTGTTATCGCTCTGTACC	441		
Dd	215	AGTTCTCTGGGTGCTGGGAGACCAACACTGACGGGAGAGTGTTATCGCTCTGTACC	274		
Qy	442	GGCTGCGACCGCTCGCTTACACCCCAGAGCTGCCGGACGCGCAAGCTGCCCTCGTGC	501		
Dd	275	GGCTGCGACCGCTCGCTTACACCCAGAGCTGCCGGAGCGCGAAGCTGSCCTCTGTGC	334		
Qy	502	TACCGGGCTGCTCATCTTGGCCCTGGCGCTTTTGGCAATGCTCTGGTGTTCACGTGG	561		
Dd	335	TCACGGCGTGTCTCATCTTGGCCCTGGCACTTTTGGCAATGCTCTGGTGTTCACGTGG	394		
Qy	562	TGACCCGACGAAGCCATGCGACCGTCACCAATCTTTATCTGCTCTTGGCGGTCA	621		
Dd	395	TGACCCGACGAAGCCATGCGACCGTCACCAATCTTTATCTGCTCTTGGCGGTCA	454		
Qy	622	GTGACCTGCTCATCACCTTCTTCTGCAATTCOCGTACCATGCTCCAGAACATTTCCGACA	681		
Dd	455	GTGACCTGCTCATCACCTTCTTCTGCAATTCOCGTACCATGCTCCAGAACATTTCCGACA	514		
Qy	682	ACTGGCTGGGGGGTGCTTTCATTTGCAAGATGGTGCCATTTTGTCCAGTCTACCGCTGTG	741		
Dd	515	ACTGGCTGGGGGGTGCTTTCATTTGCAAGATGGTGCCATTTTGTCCAGTCTACCGCTGTG	574		
Qy	742	TGACAGAAATCCTCACTATGACCTGCTTGTGTGAAAGGCACACAGGACTCTGTGCATC	801		
Dd	575	TGACAGAAATCCTCACTATGACCTGCTTGTGTGAAAGGCACACAGGACTCTGTGCATC	634		
Qy	802	CTTTTTAAATGAAGTGGCAATACACCAACCGAAGGGCTTTTACAAATGCTAGGTGTGCT	861		
Dd	635	CTTTTTAAATGAAGTGGCAATACACCAACCGAAGGGCTTTTACAAATGCTAGGTGTGCT	694		
Qy	862	GGCTGGTGGAGTCACTGTAGATCACCANTGTGGCAGTGGCAACTTGAATCAAAAT	921		
Dd	695	GGCTGGTGGAGTCACTGTAGATCACCANTGTGGCAGTGGCAACTTGAATCAAAAT	754		
Qy	922	ATGACTTCCTATATGAAAAGAAACACATCTGCTGCTTAGAAGAGTGGACACCGCTGTGC	981		
Dd	755	ATGACTTCCTATATGAAAAGAAACACATCTGCTGCTTAGAAGAGTGGACACCGCTGTGC	814		
Qy	982	ACGAGAAGATCTACACCACTTTCATCTTGTGATCTCTTCTGCTGCTCTTATGGTGA	1041		
Dd	815	ACGAGAAGATCTACACCACTTTCATCTTGTGATCTCTTCTGCTGCTCTTATGGTGA	868		
Qy	1042	TGCTTATTTCTGACGTAAAAATTTGCTTATGAATTTTGATAAGAAAAGATTTGGGGATG	1101		
Dd	869	-----	868		
Qy	1102	GTTGAGTGTCTCGAACTATTATGAAAAAGAAATGTCCAAAATAGCCAGGAAGAAAC	1161		
Dd	869	-----	880		
Qy	1162	GAGCTGCTATTATGATGATGATGAGTGGTGGCTCTCTTGTGCTGTGCTGGGCACTTCC	1221		
Dd	891	GAGCTGCTATTATGATGATGATGATGAGTGGTGGCTCTCTTGTGCTGTGCTGGGCACTTCC	940		
Qy	1222	ATGTTGTCCATATGATGATGAAATACAGTAATTTTGA AAAAGAAATATGATGATGCAAA	1281		
Dd	941	ATGTTGTCCATATGATGATGAAATACAGTAATTTTGA AAAAGAAATATGATGATGCAAA	1000		
Qy	1282	TCAGATGATTTTTGCTATCGTGCAAAATTTATGGATTTTCAA CTGTAATCCCA	1341		
Dd	1001	TCAGATGATTTTTGCTATCGTGCAAAATTTATGGATTTTCAA CTGTAATCCCA	1050		

Qy	1342	TTGTCTATGCATTATGAATGAATAAAGCTTCAAAAATAAATGTTTGTCTGCGAGTTTGTATT	1401
Db	1061	TTGTCTATGCATTATGAATGAATAAAGCTTCAAAAATAAATGTTTGTCTGCGAGTTTGTATT	1120
Qy	1402	GCATAGTAAATAAAACCTTCTCCAGCACAAAGGCGATCGAATTCAGGGAATTACAAATGA	1461
Db	1121	GCATAGTAAATAAAACCTTCTCCAGCACAAAGGCGATCGAATTCAGGGAATTACAAATGA	1180
Qy	1462	TGCGGAAGAAAGCAAAAGTTTTCCTCTCAGAGAGAAATCCAGTGGAGGAAACCAAAAGGGAAG	1521
Db	1181	TGCGGAAGAAAGCAAAAGTTTTCCTCTCAGAGAGAAATCCAGTGGAGGAAACCAAAAGGGAAG	1240
Qy	1522	CATTCACTGATGGCAACATTGAAGTCAAAATGTTGTGAAACAGACAGAGGAGAAAGAAAAGC	1581
Db	1241	CATTCACTGATGGCAACATTGAAGTCAAAATGTTGTGAAACAGACAGAGGAGAAAGAAAAGC	1300
Qy	1582	TCAAAAGACATCTTGCTCTCTTTAGGTCCTGAACTGGCTGAGAAATTCCTCTTTAGACAGTG	1641
Db	1301	TCAAAAGACATCTTGCTCTCTTTAGGTCCTGAACTGGCTGAGAAATTCCTCTTTAGACAGTG	1360
Qy	1642	GGCATTAA 1649	
Db	1361	GGCATTAA 1368	
RESULT 9			
US-09-990-940-15			
; Sequence 15, Application US/09990940			
; Publication No. US20030027252A1			
; GENERAL INFORMATION:			
; APPLICANT: Tian, Hui			
; APPLICANT: Zhao, Jiayang			
; APPLICANT: Chen, Jin-Long			
; APPLICANT: Cutler, Gene			
; APPLICANT: An, Songzhu			
; APPLICANT: Dai, Kang			
; APPLICANT: Gupte, Jamila S.			
; APPLICANT: Tularik Inc.			
; TITLE OF INVENTION: No. US20030027252A1el Receptors			
; FILE REFERENCE: 018781-007410US			
; CURRENT APPLICATION NUMBER: US/09/990,940			
; CURRENT FILING DATE: 2001-11-21			
; PRIOR APPLICATION NUMBER: US 60/252,841			
; PRIOR FILING DATE: 2000-11-22			
; PRIOR APPLICATION NUMBER: US 60/257,636			
; PRIOR FILING DATE: 2000-12-22			
; PRIOR APPLICATION NUMBER: US 60/261,377			
; PRIOR FILING DATE: 2001-01-12			
; PRIOR APPLICATION NUMBER: US 60/279,554			
; PRIOR FILING DATE: 2001-03-28			
; PRIOR APPLICATION NUMBER: US 60/280,696			
; PRIOR FILING DATE: 2001-03-29			
; NUMBER OF SEQ ID NOS: 54			
; SOFTWARE: PatentIn Ver. 2.1			
; SEQ ID NO 15			
; LENGTH: 1737			
; TYPE: DNA			
; ORGANISM: Mus sp.			
; FEATURE:			
; NAME/KEY: CDS			
; LOCATION: (1)..(1302)			
; OTHER INFORMATION: mouse G-protein coupled receptor (GPCR) TGR346a			
US-09-990-940-15			

Query Match 41.3%; Score 994.6; DB 11; Length 1737;
 Best Local Similarity 81.3%; Pred. No. 9.6e-217;
 Matches 1172; Conservative 0; Mismatches 259; Indels 12; Gaps 1;
 Qy 354 ATGAGGCGGTTTAACTTACCCGGAGCAGTTCTCTCGGTGCTGGGGACCAACCTG 413
 Db 1 ATGAGGCGCTCAACATCACCGCGAGCACTTTTCGGGTGCTGAGCGCGCAACCTG 60

QY 414 ACGGGAGAGATTCATCGCTCTGTACCGGTGCGAAGCGCTCGTCTACACCCAGAGCTG 473
DB 61 ACTCGGAAACAGTTCAATTCATCGCTATCGGCTGCGACCGCTGCTACATCCGAGCTG 120
QY 474 CCGGAGCGGCAAGCTAGTGGCCCTCGTGTCTACCGGCGTGTCTATCTTGGCCCTGCGGCTC 533
DB 121 CCGCGCGCGCTAACTAGTGGCTTTCGCTGTGCTGGAGCACTCATTTTGGCCCTGCGGCTC 180
QY 534 TTTGGCAATGCTCGGTGTTCTAGTGTGTGACCGCGCAGAGGCCATCGCGACCGTCAACC 593
DB 181 TTTGGCAACTCTCTGGTCACTATGTGTGACCGCGCAGAGGCCATCGCGACCGTCAACC 240
QY 594 AACATCTTTATCTGCTCTCTGGCCCTCAGTACCGCTGTCTCATCTCTCTCTGCAATCCC 653
DB 241 AACATCTTCTGCTCTCTGGCACTCAGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 300
QY 654 GTACCAATGCTCCAGAACATTTCCGACAACTGGTGGGGGTGTCTTCAATTTGCAAGATG 713
DB 301 GTCACGATGCTCCAGAACATCTCCGACAACTGGTGGGGGTGTCTTCAATTTGCAAGATG 360
QY 714 GTGCCATTTGTCAGTCTACCGCTGTGTGTGACAGAAATCCTCACTAGACCTGCTATGCT 773
DB 361 GTGCCCTTGTGTCAGTCTACCGCTGTGTGTGACAGAAATCCTCACTAGACCTGCTATGCT 420
QY 774 GTGAAAGGCCACCGGAGCTTGTGCTCTCTTTTAAATGAAGTGGCAATACACCAACCGA 833
DB 421 GTTGAGAGGCCACCGGAGCTCACTCATCTCTTTTAAATGAAGTGGCAATACACCAACCGA 480
QY 834 AGGCTTTCAAGTCTAGTGTGGTCTGGCTGTGGCGATCATCTGTTAGGATCAACCGATG 893
DB 481 AGGCTTTCAAGTCTAGTGTGGTCTGGTGTGGCGATCATCTGTTAGGATCAACCGATG 540
QY 894 TGGCAGCGTCAACACTTGAGTCAAAATGACATCTCTATATGAAATGAAGGAACATCTGCG 953
DB 541 TGGCAGCTCAACCGCTCGAGTAAAGTATGACTTCTCTATGAGAAAGAACATCTGCTCG 600
QY 954 TGCTTAGAAGTGGACAGCCCTGTGCACCAAGAGATCTACACCACTTCATCCTTGTGTC 1013
DB 601 TGTTTGAAGAGTGGCGAGCCCATGCACAGAGAAATCTACACCACTTCATCCTGCTC 660
QY 1014 ATCT 1073
DB 661 ATCT 720
QY 1074 CTCTTGATTAAGAAAGAGTGGGATGTTTGGGATGTTTGGGATGTTTGGGATGTTTGGG 1133
DB 721 CTCTGGATCAAGAGAGAGTGGGAGACAGTTCAGACATTCAGACTATCCAGGGAGAA 780
QY 1134 ATGTCCAAATATGCGAGGAAGAAACGAGCTGTCTATATGATGTGTGACAGTGTGTGCT 1193
DB 781 ATGTCCAAATATGCGAGGAAGAAAGCGGCTGTCTGTTATGATGTGTGACAGTGTGTGCT 840
QY 1194 CTCTTGT 1253
DB 841 CTCTTGT 900
QY 1254 TTTGAAAGAGGATATGATGATGTCAATCAAGATGATTTTGTCTATCGTCAAAATATT 1313
DB 901 TTTGAAAGAGGATATGATGATGTCAATCAAGATGATTTTGTCTATCGTCAAAATATT 960
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DB 961 GGCTTTTCCAACTCCATCTGTAATCCCAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1020
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DB 1021 AAGAAATTTTGTCTGCGATTTGTTTATGTCATAGTAATAAATCACTCTCTCCAGCAAA 1080
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DB 1081 AAGCCTGGAATTTCTGGGATTTCAATGATGAAAAGAGAGCAAGTTTATCAGATCAAG 1140
QY 1494 AATCCAGTGGAGAAACCAAGAGAGAGCAATTCAGTGTGGAACATTCAGTGAATTCAGTGAATTC 1553

DB 1141 CGTCCAGTGGCGAGCGCAAGGAGACTTATTTCAGCGATGCCAAGCTTGATGTCAATTTG 1200
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DB 1201 TGTGAGCAGCAGGAGGAGAAAGGCAACTCAAGCGACAGCTTGCCTTCTTTAGTCTGAA 1260
QY 1614 CTGGCTGAGAAATCTCTCTTTAGACAGTGGCATTAAATAACAATATCTTCATAATTAA 1673
DB 1261 CTTTCTGAAACTCTACTTTCGCGAGTGGACATGACTGTAATGATATCTCATAGCTAA 1320
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DB 1321 TATCAITTTGAT-----GGAAAGTATTATTAGCAAAGGTCAGGACTATTTT 1368
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DB 1369 TTTAAATGACAAAGAGAAACAAAGACATGTTTTCATTAAATGAACATAATACATAAC 1428
QY 1794 GCT 1796
DB 1429 ACT 1431

RESULT 10
US-09-990-940-17
; Sequence 17, Application US/09990940
; Publication No. US20030027252A1
; GENERAL INFORMATION:
; APPLICANT: Tian, Hui
; APPLICANT: Zhao, Jiaqiang
; APPLICANT: Chen, Jin-Long
; APPLICANT: Cutler, Gene
; APPLICANT: An, Songzhu
; APPLICANT: Dai, Kang
; APPLICANT: Gupte, Jamila S.
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: No. US20030027252A1e1 Receptors
; FILE REFERENCE: 018781-007410US
; CURRENT APPLICATION NUMBER: US/09/990,940
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/252,841
; PRIOR FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: US 60/257,636
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 60/261,377
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 60/279,554
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 60/280,696
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 1772
; TYPE: DNA
; ORGANISM: Mus sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1251)
; OTHER INFORMATION: mouse G-protein coupled receptor (GPCR) TGR346b
US-09-990-940-17

Query Match 38.6%; Score 932; DB 11; Length 1772;
Best Local Similarity 92.0%; Pred. No. 1.9e-202;
Matches 1138; Conservative 0; Mismatches 235; Indels 15; Gaps 5;
QY 359 GGCGCTTAAACATTAACCGGAGCAGTTCTCTCGGCTGTGCGGACCAACACCTGACGCG 418
DB 3 GTCTGTGAACCTTGACCGCGGAGCAGCTCTCGGCTGTGCGCTGACACACCTGACGCG 62
QY 419 GGAGCACTTCATCGCTCTGTACCGGCTGCGACCGCTCTGTACACCCAGAGCTGCCGG 478

Db 63 CGCTCAGTTCATCGGCGCACTATGAGGCTGGGCCACTGGTGTCTACCCCGCAGCTTCCCGC 122
Qy 479 ACGGCCCAAGCTGGCCCTCGTCTCTACCGCGGTGCTCATCTTCGCCCTGGCGCTCTTTGG 538
Db 123 GCGGCCCAAGCTGGCCCTCGTCTCTCGGTGGCGATGCTCATCTTTGGCCCTGGCGCTCTTTGG 182
Qy 539 CAATGCTCTGGTGTCTACGTGGTGAACCGCGAGCGCAAGGCCCATGGCCACCGTCACCAACAT 598
Db 183 CAACGCCCTGGTGTCTATGTTGACCGCGAGCAAGGCCCATGGCCACCGTCACCAACAT 242
Qy 599 CTTTATCTGCTCTTTGGCGCTCAGTGAAGTCTGCTCATCTCTCTGATCTCCCGTAC 658
Db 243 CTTTATCTGCTCTTTGGCGCTCAGTGAAGTCTGCTCATCTCTCTGATCTCCCGTAC 302
Qy 659 CATGCTCCAGAACATTTCCGAACTGGCTGGGGGGTGTCTTTTCTTTCAGATGGTGCC 718
Db 303 CATGCTCCAGAACATTTCCGAACTGGCTGGGGGGTGTCTTTTCTTTCAGATGGTGCC 362
Qy 719 ATTGTCCAGTCTACCGCTGTTGTGACAGAAATCCTCTATGACCTGCTGATGTGTGGA 778
Db 363 ATTGTCCAGTCTACCGCTGTTGTGACAGAAATCCTCTATGACCTGCTGATGTGTGGA 422
Qy 779 AAGGACACGAGGACTTGGCACTCTTTTAAATGAAGTGGCAATACACCAACCGAAGGC 838
Db 423 AAGGACACGAGGACTTGGCACTCTTTTAAATGAAGTGGCAATACACCAATCAAGAGC 482
Qy 839 TTTTCAATGTAGTGTGTGTGGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 898
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Qy 899 GTGCAACAACTTGATGATCAAAATGATCTTCTTATGAAAGGAACACATCTGTGCTT 958
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RESULT 11

US-10-017-161-1163
; Sequence 1163, Application US/10017161
; Publication No. US20030143668A1
; GENERAL INFORMATION:
; APPLICANT: SUMA, MAKINO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ABURATANI, HIROYUKI
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 084335/0152
; CURRENT APPLICATION NUMBER: US/10/017,161
; PRIOR FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: JP 2001/246789
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 2430
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1163
; LENGTH: 940
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: source
; LOCATION: (1)..(940)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (201)..(740)
US-10-017-161-1163

Query Match 22.4%; Score 542; DB 12; Length 940;
Best Local Similarity 100.0%; Pred. No. 1.5e-113;
Matches 542; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 274 CCGAAGCCTTCCCGCGGCTGATCCAGTAGAGAGAGGAGGCGGCTCCGGTGTGTC 333
Db 121 CCGAAGCCTTCCCGCGGCTGATCCAGTAGAGAGAGGAGGCGGCTCCGGTGTGTC 180
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Db 181 CGTCCCGGAGCGCACAGCAATGAGGCGCTTAACTATCCCGGAGCAGTTCTCTCGGC 240
Qy 394 TGCTGCGGAGCCACACCTGACGCGGAGCAGTTTATCGTCTGTACCGGCTGCGACCGC 453
Db 241 TGCTGCGGAGCCACACCTGACGCGGAGCAGTTTATCGTCTGTACCGGCTGCGACCGC 300
Qy 454 TCGTCTACCCCGAGAGCTGCGGAGCGGCGCAAGCTGTGGCCCTCTGCTCTACCGGCTGTC 513


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Db 23432 CCAGCTACTCGGGAGGCTGAGGCGAGGAGATGGCGTGAACCCGGGAGCGGAGCTTGCAG 23491
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Qy 2133 TGTCCGAGATCATGCCACTCCAGCTCCAGCCTGGGCGAAAGAGCGAGACTCCCGTCTCA 2192
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Db 23552 AAAAAAACAAAAAACAAAAAACAAAAAACAAAA 23584
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Search completed: October 29, 2003, 12:05:06
Job time : 669 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 29, 2003, 05:35:04 ; Search time 648 Seconds
(without alignments)
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Title: US-10-070-241B-2

Perfect score: 2415

Sequence: 1 gccagagggccaggaccct.....aaaaaaaaaaaaaaaaaagg 2415

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_19Jun03.*

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- 25: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	2412	99.9	2415	22 AAF81819	Human G protein-co
2	2390.2	99.0	2448	25 AAF81819	Human G protein co
3	2389.6	98.9	2411	21 AAA23435	cDNA encoding huma
4	1668.4	69.1	1710	24 ABK14957	Human neuroepitide
5	1296	53.7	1296	22 AAH49502	Human GTP-binding
6	1296	53.7	1296	22 AAC87690	Human G protein-co
7	1296	53.7	1296	24 ABK6287	Human TGR346 cDNA.
8	1296	53.7	1296	24 ABK14956	Human neuroepitide

9	1294.4	53.6	1296	21 AAD01136	Human orphan G pro
10	1294.4	53.6	1296	21 AAA46037	Human G protein co
11	1293	53.5	1293	22 AAF81818	Human G protein-co
12	1289.6	53.4	1296	21 AAA46115	Human G protein co
13	1078.4	44.7	1368	25 AB242861	Human G protein-co
14	994.6	41.2	1737	24 ABR66292	Mouse TGR346a cDNA
15	932	38.6	1772	24 ABR66293	Mouse TGR346b cDNA
16	737	30.5	741	24 AAS98050	Human DNA for pote
17	500	20.7	511	21 AAD01143	Human orphan G pro
18	500	20.7	511	21 AAA46044	Human G protein co
19	309	12.8	432	22 AAI70302	Human GPCR-like pr
20	309	12.8	432	24 ABL42350	Human galanin rece
21	309	12.8	432	24 AAS98092	Human DNA for pote
22	251.4	10.4	114783	22 AAD08215	Human genome from
23	251.2	10.4	506	22 ABA15628	Human nervous syst
24	251	10.4	3178	22 AAK80500	Human immune/haema
25	249.8	10.3	501	22 ABA15627	Human immune/haema
26	249.8	10.3	31871	23 ABK42516	Genomic sequence #
27	249.8	10.3	40742	22 AAK68089	Human immune/haema
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31	249.2	10.3	267156	24 ABL68560	Kidney cancer rela
32	249	10.3	333	22 AAK66811	Human immune/haema
33	249	10.3	333	22 AAK66812	Human immune/haema
34	249	10.3	333	22 AAK66613	Human immune/haema
35	248.4	10.3	249999	25 AB280329	Human tramdorin ge
36	248	10.3	331	22 AAK78782	Human immune/haema
37	248	10.3	4124	22 AAS01154	5'-untranslated re
38	248	10.3	32145	22 AAK68491	Human immune/haema
39	248	10.3	32145	22 AAK68575	Human immune/haema
40	248	10.3	144460	21 AAZ93815	Olfactory receptor
41	247.8	10.3	31474	22 AAL05461	Human reproductive
42	247.8	10.3	31474	23 ABL98314	Human testicular a
43	247.4	10.2	11360	22 AAL03820	Human reproductive
44	247.4	10.2	11360	22 AAL04727	Human reproductive
45	247	10.2	17570	25 ABZ74059	Secreted protein g

ALIGNMENTS

RESULT 1
AAAF81819
ID AAF81819 standard; cDNA; 2415 BP.

AC AAF81819;

XX 05-JUN-2001 (first entry)

XX Human G protein-coupled receptor protein AQ27 encoding cDNA.

XX Human; G protein-coupled receptor; AQ27; nootropic; neuroprotective;
XX hypotensive; antirheumatic; antiallergic; cardiant; antianaginal;
XX abortifacient; gene therapy; Alzheimer's disease; hypertension;
XX pregnancy termination; rheumatism; allergy; angina pectoris; ss.

XX Homo sapiens.

PH Key Location/Qualifiers
CDS 354..1649

FT FT /*tag= a
FT FT /product= "AQ27"
FT FT /note= "G protein coupled receptor"

XX WO200116316-A1.

XX 08-MAR-2001.

XX 24-AUG-2000; 2000WO-JP05684.

XX 27-AUG-1999; 99JP-0241530.

XX

(TAKE) TAKEDA CHEM IND LTD.
 Watanabe T, Kikuchi K, Shintani Y;
 WPI; 2001-226689/23.
 P-PSDB; AAB74773.
 Human brain-originated guanosine triphosphate protein-coupled receptor,
 its salt and encoded gene, useful in (gene) diagnosis and development
 of preventives and remedies for e.g. Alzheimer disease, hypertension
 and rheumatism -
 Disclosure; Fig 1-2; 84pp; Japanese.
 The present sequence encodes a human G protein-coupled receptor
 designated AQ27. AQ27 has nootropic, neuroprotective, hypotensive,
 antirheumatic, anti-allergic, cardiant, anti-anginal and abortifacient
 activities. AQ27 can be used as a G protein-coupled receptor protein
 agonist, G-protein-coupled receptor signal transducer and in gene
 therapy. AQ27 can be sued in the diagnosis and development of
 preventives and remedies for diseases associated with dysfunction of
 AQ27 e.g. Alzheimer's disease, hypertension, pregnancy termination,
 rheumatism, allergy and angina pectoris.
 Sequence 2415 BP; 670 A; 579 C; 561 G; 602 T; 3 other;

Query Match 99.9%; Score 2412; DB 22; Length 2415;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2415; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 61 CCTTAGGAGAGCAAGGAAGAACTTTATTTGAACCGGAACTTTTGGTCTCATGAG 120

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 DB 121 ATCGAGTCTCCAGTGTCTTGGCTTCCCGCTCTTTATCGTGGTGTGATCCCTGAGCTG 180

QY 181 CTCTCTTTCCGAACTCCCGGGGTGACGCTAGAGCCCTCCCGCGCGGTGACTCCAG 240
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 DB 301 CGGATGGCCAGGACAGTAGCGGGCGGTGGCCCGCGTCCCGGAGGCGCAGCAATGCGAG 360

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 DB 361 CGCTTAACTATCCCGGAGAGTCTCTCGGCTGCTCGGAGCACAACCTGACGCGGG 420

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QY 2161 GCCTGGGGAAGAGCGAGACTCCCGTCTCAAAAAATTTTGAANAATTCGTAA 2220
Db 2161 GCCTGGGGAAGAGCGAGACTCCCGTCTCAAAAAATTTTGAANAATTCGTAA 2220
QY 2221 CCATCTTTTAAGTATTTTCACTGGATTTTAAAAATCTGTACAGAAATCAGGGTTCT 2280
Db 2221 CCATCTTTTAAGTATTTTCACTGGATTTTAAAAATCTGTACAGAAATCAGGGTTCT 2280
QY 2281 TAGCTAGAGTTTCTCCACGAGTCACTGTAATGTGACTATGATTCAGATTGAA 2340
Db 2281 TAGCTAGAGTTTCTCCACGAGTCACTGTAATGTGACTATGATTCAGATTGAA 2340
QY 2341 TAAGAAATAAATAATATCTTCTTCTTGAANAATTTTAAAAATTTTAAAAATTTTAAAA 2400
Db 2341 TAAGAAATAAATAATATCTTCTTCTTGAANAATTTTAAAAATTTTAAAAATTTTAAAA 2400
QY 2401 AAAAAAAAAAAAAAGG 2415
Db 2401 AAAAAAAAAAAAAAGG 2415

RESULT 2

ABS57631
ID ABS57631 standard; cDNA; 2448 BP.

XX AC

XX AC

XX AC

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XX AC

14-FEB-2003 (first entry)

Human G protein coupled receptor HGPBMY2 cDNA SEQ ID 16.

Human: G-protein coupled receptor; HGPBMY1; HGPBMY2; immunosuppressive; cardiant; neuroprotective; antiinflammatory; cytostatic; vulnery; vaccine; gene therapy; autoimmune; cardiovascular; neural; reproductive; haematopoietic; pulmonary; gastrointestinal; proliferation; cell cycle; birth defect; aberrant phosphorylation; acute phase response; receptor; signal transduction; hyperimmune activity; inflammatory; hypercongenital; necrotic lesion; wound; organ transplant rejection; gene; disorder; ss.

Homo sapiens.

Key Location/Qualifiers

FF 359..1654

FT /*tag= a

FT /product= "HGPBMY2"

FT

XX WO200268591-A2.
XX 06-SEP-2002.
XX 22-FEB-2002; 2002WO-US05281.
XX 23-FEB-2001; 2001US-370792P.
XX 23-FEB-2001; 2001US-370793P.
XX 06-JUN-2001; 2001US-296427P.
XX (BRIM) BRISTOL-MYERS SQUIBB CO.
XX Feder J, Ramanathan C, Nelson T, Mintier G, Cacace A, Barber L;
PI Kornacker M, Bol D;
XX WPI; 2003-058304/05.
XX P-PSDB; ABG73503.
XX New human HGPBMY1 or HGPBMY2 polynucleotide and polypeptide, useful
PT preventing, treating or ameliorating a disorder e.g., wound,
PT cardiovascular disorder or transplant rejection
XX Claim 1; Figure 6; 316pp; English.
XX This invention describes the novel human G-protein coupled receptors
CC (GPCR's), HGPBMY1 or HGPBMY2 which have immunosuppressive, cardiant,
CC neuroprotective, antiinflammatory, cytostatic and vulnery activity
CC and can be used in vaccines or for gene therapy. Pharmaceutical
CC compositions comprising HGPBMY1 or HGPBMY2 polypeptides or their
CC agonists or antagonists or modulators, or a HGPBMY1- or
CC HGPBMY2-specific antibody are useful for preventing, treating or
CC ameliorating a medical condition comprising autoimmune, cardiovascular,
CC neural, reproductive, haematopoietic, pulmonary, gastrointestinal or
CC proliferating disorder, a cell cycle or birth defect, a disorder related
CC to aberrant phosphorylation, acute phase responses or signal transduction
CC or to hyperimmune activity, an inflammatory or hypercongenital condition,
CC a necrotic lesion, a wound, organ transplant rejection or a condition
CC related to organ transplant rejection. This sequence encodes the human
CC HGPBMY2 protein described in the disclosure of the invention.
XX SQ Sequence 2448 BP; 665 A; 597 C; 575 G; 611 T; 0 other;
Query Match 99.0%; Score 2390.2; DB 25; Length 2448;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 2392; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 7 GGGCCAGGACCCCTAGCTGGCGCTCCAGACCCAGACCCGCGCGCTCGCCTTAG 66
Db 12 GGGCCAGGACCCCTAGCTGGCGCTCCAGACCCAGACCCGCGCGCTCGCCTTAG 71
QY 67 GGAAGAGCAAGGGAAGAACTTTATTGAACCGCGAACATTTTGGTCACTGAGATCGAG 126
Db 72 GGAAGAGCAAGGGAAGAACTTTATTGAACCGCGAACATTTTGGTCACTGAGATCGAG 131
QY 127 TCTCCAGTGTCTTGGCTTCCCGCCTCTTTATCGTGGGTTTATCCTCAGCTGCTCTCC 186
Db 132 TCTCCAGTGTCTTGGCTTCCCGCCTCTTTATCTTGGGTTTATCCTCAGCTGCTCTCC 191
QY 187 TTTCCGAACTTCCCGGGGTGAGCTAGAGCCCTCCCGCGGTGACTCCAGAGTAGA 246
Db 192 TTTCCGAACTTCCCGGGGTGAGCTAGAGCCCTCCCGCGGTGACTCCAGAGTAGA 251
QY 247 GGAAGGAGCGCGCTCCCGCTGCTCCCGGAGCCCTGCTGCCCGGAGATGGGATG 306
Db 252 GGAAGGAGCGCGCTCCCGCTGCTGCCCGGAGCCCTGCTGCCCGGAGATGGGATG 311
QY 307 GCCAGCCAGTAGCGGCGGTGGCCCGCGTCCCGGAGCGCACAGCAATGCGGGCTTA 366
Db 312 GCCAGCCAGTAGCGGCGGTGGCCCGCGTCCCGGAGCGCACAGCAATGCGGGCTTA 371
QY 367 ACATTACCCCGAGCAGTTCTCTCGGTGCTGTCGGGACCAACCTGACGCGGAGCAGT 426

Db 372 ACATTACCCCGAGCAGTTCTCTCGGCTGCTGCGGACCAACAACCTGACGGGAGCAGT 431
Qy 427 TCATCGCTCTCTACCGGCTGCGACCGCTCGTCTACACCCCGAGAGTGC CGGAGCGGCA 486
Db 432 TCATCGCTCTCTACCGGCTGCGACCGCTCGTCTACACCCCGAGAGTGC CGGAGCGGCA 491
Qy 487 AGCTGGGCCCTCGTGCTACCGGCGTGCTCATCTTCGCGCCCTGCGCGCTCTTTGGCAATGCTC 546
Db 492 AGCTGGGCCCTCGTGCTACCGGCGTGCTCATCTTCGCGCCCTGCGCGCTCTTTGGCAATGCTC 551
Qy 547 TGGTGTTCTAGTGGTGACCGCGACGAGGCGCATGCGCACCGTCCACCAACATCTTTATCT 606
Db 552 TGGTGTTCTAGTGGTGACCGCGACGAGGCGCATGCGCACCGTCCACCAACATCTTTATCT 611
Qy 607 GCTCCTTGGCGCTCAGTGACCTGCTCATCACTTCTTCTGCAATCCCGCTCAACATGCTCC 666
Db 612 GCTCCTTGGCGCTCAGTGACCTGCTCATCACTTCTTCTGCAATCCCGCTCAACATGCTCC 671
Qy 667 AGAACATTCGACMACTGGCTGGGGGTGCTTTCATTTGCAAGATGGTGCCATTTGTC 726
Db 672 AGAACATTCGACMACTGGCTGGGGGTGCTTTCATTTGCAAGATGGTGCCATTTGTC 731
Qy 727 AGTCTACCGCTGTTGTGACAGAAATCCCTCACTATGACCTGCATTCGCTGGAAGGCACC 786
Db 732 AGTCTACCGCTGTTGTGACAGAAATCCCTCACTATGACCTGCATTCGCTGGAAGGCACC 791
Qy 787 AGGAATTTGTCATCTCTTTTAAATGAAGTGGCAATACACCAACCGAGGCTTTCACAA 846
Db 792 AGGGACTTGTGCATCTCTTTTAAATGAAGTGGCAATACACCAACCGAGGCTTTCACAA 851
Qy 847 TGCTAGTGTGCTGCTGGCTGGCAGTCATGCTAGGATCACCATCCATGTGGCACTGCAAC 906
Db 852 TGCTAGTGTGCTGCTGGCTGGCAGTCATGCTAGGATCACCATCCATGTGGCACTGCAAC 911
Qy 907 AACTTGAGATCAATATGACTTCTTATGAAAGGAACACATCTGCTGTAGAGAGT 966
Db 912 AACTTGAGATCAATATGACTTCTTATGAAAGGAACACATCTGCTGTAGAGAGT 971
Qy 967 GGACAGCCCTGTGCACAGAGATCTACACACCTTCATCCTTGTCACTCTTCTCTCC 1026
Db 972 GGACAGCCCTGTGCACAGAGATCTACACACCTTCATCCTTGTCACTCTTCTCTCC 1031
Qy 1027 TGCCTCTTATGCTGATGCTTATCTGACAGTAAATTTGGTATGAACTTTGGATAAGA 1086
Db 1032 TGCCTCTTATGCTGATGCTTATCTGACAGTAAATTTGGTATGAACTTTGGATAAGA 1091
Qy 1087 AAAGAGTTGGGATGGTTCAGTGTCTGAACTATTTCATGGAAGAAATGTCGAAATAG 1146
Db 1092 AAAGAGTTGGGATGGTTCAGTGTCTGAACTATTTCATGGAAGAAATGTCGAAATAG 1151
Qy 1147 CCAGAGAGAGAAACGAGCTGTCAATATGATGGTGACAGTGGTGCTCTTTGCTGTGT 1206
Db 1152 CCAGAGAGAGAAACGAGCTGTCAATATGATGGTGACAGTGGTGCTCTTTGCTGTGT 1211
Qy 1207 GCTGGGACCACTTCATGCTGTCATATGATGATTTGAATCAGTAATTTTGAAGGAAT 1266
Db 1212 GCTGGGACCACTTCATGCTGTCATATGATGATTTGAATCAGTAATTTTGAAGGAAT 1271
Qy 1267 ATGATGATGTCACAATCAAGATGATTTTGTCTGTCGCAAAATTTATGATTTTCCAAT 1326
Db 1272 ATGATGATGTCACAATCAAGATGATTTTGTCTGTCGCAAAATTTATGATTTTCCAAT 1331
Qy 1327 CCATCTGTAATCCGATTTGCTATGCAATTTATGATGAAATTTCAAAAAAATGTTTGT 1386
Db 1332 CCATCTGTAATCCGATTTGCTATGCAATTTATGATGAAATTTCAAAAAAATGTTTGT 1391
Qy 1387 CTGCAGTTTGTATGCTAGTAAATAAAGCTTCTCCAGCAACAAAGGATGGAAT 1446
Db 1392 CTGCAGTTTGTATGCTAGTAAATAAAGCTTCTCTCCAGCAACAAAGGATGGAAT 1451
Qy 1447 CAGGAATTTAATGATGCGGAGGAAAGCAAAAGTTTTCCTCAGAGAGAAATCCAGTGGAGG 1506
Db 1452 CAGGAATTTAATGATGCGGAGGAAAGCAAAAGTTTTCCTCAGAGAGAAATCCAGTGGAGG 1511

Qy 1507 AAACCAAGAGAGAGCAATTCAGTGATGGCAACATTTGAAGTCABAATTTGTGTGAACAGACAG 1566
Db 1512 AAACCAAGAGAGAGCAATTCAGTGATGGCAACATTTGAAGTCABAATTTGTGTGAACAGACAG 1571
Qy 1567 AGGAGAGAGAGAGAGCTCAAAACGACATCTTGTCTCTCTTTAGGTCTGAACTGGCTGAGAAAT 1626
Db 1572 AGGAGAGAGAGAGAGCTCAAAACGACATCTTGTCTCTCTTTAGGTCTGAACTGGCTGAGAAAT 1631
Qy 1627 CTCCTTTAGACAGTGGCATTAAATTAACAATATCTTCAATAATTAATGATGATGATGATGAT 1686
Db 1632 CTCCTTTAGACAGTGGCATTAAATTAACAATATCTTCAATAATTAATGATGATGATGATGAT 1691
Qy 1687 GTAACCCAAAGAGAGAAATTTTGAACAAAGTCAAAATCTCTTTAAATTTCTTAAAGATG 1746
Db 1692 GTAACCCAAAGAGAGAAATTTTGAACAAAGTCAAAATCTCTTTAAATTTCTTAAAGATG 1751
Qy 1747 ATGACAAAGAGAGAGAAACAAATCATGTTTCCATTTAAATAACACAGAGCTAGTCCAAAGT 1806
Db 1752 ATGACAAAGAGAGAGAAACAAATCATGTTTCCATTTAAATAACACAGAGCTAGTCCAAAGT 1811
Qy 1807 CAGTGATGTTTCAACCAATNGATCAATCAATTTAACANATTTCTGTGTTCTCTTCTCAT 1866
Db 1812 CAGTGATGTTTCAACCAATNGATCAATCAATTTAACANATTTCTGTGTTCTCTTCTCAT 1871
Qy 1867 TCCCACTGCTTCACTTGAATGAGCTTTAAAAAAGCAACATGGAAGGCCAGGACGCTGGCT 1926
Db 1872 TCCCACTGCTTCACTTGAATGAGCTTTAAAAAAGCAACATGGAAGGCCAGGACGCTGGCT 1931
Qy 1927 CATGCCCTGTAATCCAGACACTTTGGAGGCGCTAGACGGGCGGATCAGAGGTGAGGAGAT 1986
Db 1932 CATGCCCTGTAATCCAGACACTTTGGAGGCGCTAGACGGGCGGATCAGAGGTGAGGAGAT 1991
Qy 1987 CAACCACTCCTGGCTAAACACGCTGAAACCCCATCTCTGCTTAAATAACAAAAATTTAGCC 2046
Db 1992 CAACCACTCCTGGCTAAACACGCTGAAACCCCATCTCTGCTTAAATAACAAAAATTTAGCC 2051
Qy 2047 GGGCGTGGTGGCGGCGACCTGTAGTCCAGCTACTTTGGAGGCTCAGGCGGAGAAATGGT 2106
Db 2052 GGGCGTGGTGGCGGCGACCTGTAGTCCAGCTACTTTGGAGGCTCAGGCGGAGAAATGGT 2111
Qy 2107 GTAAACCCGGAGGCGGAGCTTCAGTGATCCAGATCATGCCAGTGCATCCAGGCTGG 2166
Db 2112 GTAAACCCGGAGGCGGAGCTTCAGTGATCCAGATCATGCCAGTGCATCCAGGCTGG 2171
Qy 2167 GCGAAGAGCGAGACTCCCGCTCTCAAAAAAATTTTTTGAATAATTCCTTAACCATAC 2226
Db 2172 GCGAAGAGCGAGACTCCCGCTCTCAAAAAAATTTTTTGAATAATTCCTTAACCATAC 2231
Qy 2227 TTTTAAAGATTTTCAAGTGGATTTTAAATAATCTTGTACAGAAATCAGGGTTCTTAGCTA 2286
Db 2232 TTTTAAAGATTTTCAAGTGGATTTTAAATAATCTTGTACAGAAATCAGGGTTCTTAGCTA 2291
Qy 2287 GCAGTTTCTCCAGCGAGTCACTGATGACATGATGATGATGATGATGATGATGATGATGAT 2346
Db 2292 GCAGTTTCTCCAGCGAGTCACTGATGACATGATGATGATGATGATGATGATGATGATGAT 2351
Qy 2347 AATAAATAATATCTCTCTCTGNAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAA 2404
Db 2352 AATAAATAATATCTCTCTCTGNAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAA 2409

RESULT 3
AAA23435

ID AAA23435 standard; cDNA; 2411 BP.

XX AAA23435;

XX 19-JUN-2000 (first entry)

XX cDNA encoding human secreted protein vc38_1, SEQ ID NO:25.

XX Human; secreted protein; cancer; tumour; cardiovascular disorder;

Qy	1141	AAATAGCCAGGAAGAGAAACGAGCTGTCAATTATGATGGTGACAGTGGTGCTCTCTTTG	1200
Db	1157	AAATAGCCAGGAAGAGAGAAACGAGCTGTCAATTATGATGGTGACAGTGGTGCTCTCTTTG	1216
Qy	1201	CTGTGTGCTGGGCACCAATTCATGCTGTCCATATGATGATGATGAATACAGTAATTTTGAAA	1260
Db	1217	CTGTGTGCTGGGCACCAATTCATGCTGTCCATATGATGATGATGAATACAGTAATTTTGAAA	1276
Qy	1261	AGGAATATGATGATGTCACAAATCAAGATGATTTTTTGTATCGTGCAAAATATTGGATTTT	1320
Db	1277	AGGAATATGATGATGTCACAAATCAAGATGATTTTTTGTATCGTGCAAAATATTGGATTTT	1336
Qy	1321	CCAACTCATCTGPAATCCCAATTGTCATGCAATTATGAATGAAAACTTCAAAAAAATG	1380
Db	1337	CCAACTCATCTGPAATCCCAATTGTCATGCAATTATGAATGAAAACTTCAAAAAAATG	1396
Qy	1381	TTTTGTCTGCAGTTTGTATTGTCATAGTAATAAACAATCTCTCCAGCACAAGGCATG	1440
Db	1397	TTTTGTCTGCAGTTTGTATTGTCATAGTAATAAACAATCTCTCCAGCACAAGGCATG	1456
Qy	1441	GAATTCAGGAATPACAATGATCGGAGAGAAAGCAAAAGTTTTCCTCCAGAGAAATCCAG	1500
Db	1457	GAATTCAGGAATPACAATGATCGGAGAGAAAGCAAAAGTTTTCCTCCAGAGAAATCCAG	1516
Qy	1501	TGGAGGAAACCAAGGAGAGACATTCAGTGATGCGACATTTGAATCAAAATGTGTGAAC	1560
Db	1517	TGGAGGAAACCAAGGAGAGACATTCAGTGATGCGACATTTGAATCAAAATGTGTGAAC	1576
Qy	1561	AGACAGAGGAGAGAAAAAGCTCAAAACGACATCTTGTCTCTTTAGTGCTCGAACTGGCTG	1620
Db	1577	AGACAGAGGAGAGAAAAAGCTCAAAACGACATCTTGTCTCTTTAGTGCTCGAACTGGCTG	1636
Qy	1621	AGAAATCTCTTTAGACAGTGGGCATTAATTATPACAAATATCTTCAATAATTAATGCCCTT	1680
Db	1637	AGAAATCTCTCTTTAGACAGTGGGCATTAATTATPACAAATATCTTCAATAATTAATGCCCTT	1696
Qy	1681	CAGATTGTAAACCCAAAGAGAAAAATTTTTGAGCAAAAGGTCAAATATCTCTTTTAATTCCT	1740
Db	1697	CAGATTGTAAACCCAAAGAGAAAAATTTTTGAGCAAAAGGTCAAATATCTCTTTTAATTCCT	1756
Qy	1741	AAGATGATGACAAGAGAAAAACAAATCATGTTTCCATTAAAAATGACAGGCTAGTC	1800
Db	1757	AAGATGATGACAAGAGAAAAACAAATCATGTTTCCATTAAAAATGACAGGCTAGTC	1816
Qy	1801	CAAGTCAGTGATGTTTAAACCAATNGATCACAATCATTTTAAACAAATTTCTGTGTTCCCT	1860
Db	1817	CAAGTCAGTGATGTTTAAACCAATNGATCACAATCATTTTAAACAAATTTCTGTGTTCCCT	1876
Qy	1861	TCTCATTTCCCACTGCTTCACTTGACTAGCTTTAAAAAGCAACATGAAGCCAGGCACG	1920
Db	1877	TCTCATTTCCCACTGCTTCACTTGACTAGCTTTAAAAAGCAACATGAAGCCAGGCACG	1936
Qy	1921	GTGCTCATGCTGTAAATCCAGCACATTTGGAGGCGCTAGACGGCGCGATCAAGAGTCA	1980
Db	1937	GTGCTCATGCTGTAAATCCAGCACATTTGGAGGCGCTAGACGGCGCGATCAAGAGTCA	1996
Qy	1981	GGAGATCAAAACCAATCTGGGTAACAAGTGAAACCCCACTCTGCTTAAAAATACAAAAA	2040
Db	1997	GGAGATCAAAACCAATCTGGGTAACAAGTGAAACCCCACTCTGCTTAAAAATACAAAAA	2056
Qy	2041	TTAGCCGGCGGTGTGGCGGCGCACTGTAGTCCAGCTACTTGGAGGCGCTCAGCGGGAG	2100
Db	2057	TTAGCCGGCGGTGTGGCGGCGCACTGTAGTCCAGCTACTTGGAGGCGCTCAGCGGGAG	2116
Qy	2101	AATGGTGTGAACCCGGAGGCGGAGCTTGCAAGTATCCGAGATCATGCCACTGCATCCCA	2160
Db	2117	AATGGTGTGAACCCGGAGGCGGAGCTTGCAAGTATCCGAGATCATGCCACTGCATCCCA	2176
Qy	2161	GCCTGGCGGAAAGACGAGACTCCCGCTCTCAAAAAAATTTTTTTTGAATAATTCGTAAA	2220
Db	2177	GCCTGGCGGAAAGACGAGACTCCCGCTCTCAAAAAAATTTTTTTTGAATAATTCGTAAA	2236

Qy	2221	CCATACCTTTTAAGATTATTTTCAGTGGATTTTTTAAAAAATCTGTACAGAAATCAGGGTTCT	2288
Db	2237	CCATACCTTTTAAAGATTATTTTCAGTGGATTTTTTAAAAAATCTGTACAGAAATCAGGGTTCT	2296
Qy	2281	TAGCTAGCAGTTTTTCTCCACACGAGTCACCTGTAATGTGACTATATGATTGCTAGATTGAA	2340
Db	2297	TAGCTAGCAGTTTTTCTCCACACGAGTCACCTGTAATGTGACTATATGATTGCTAGATTGAA	2356
Qy	2341	TAGAAAAATAAATAATATCTTCTCTTGNAAAAAATAAAAAAAAAAAAAA 2395	
Db	2357	TAGAAAAATAAATAATATCTTCTCTTGNAAAAAATAAAAAAAAAAAAAA 2411	
RESULT 4			
ABK14957			
ID	ABK14957	standard; DNA; 1710 BP.	
XX			
XX	ABK14957;		
DT	08-MAY-2002	(first entry)	
XX			
DE	Human neuropeptide Y-like GPCR (NPY-like GPCR) DNA sequence.		
XX			
KW	Human; neuropeptide Y-like G protein-coupled; receptor; antibody;		
KW	NPY-like GPCR; anorectic; antidiabetic; tranquilizer; hypertensive;		
KW	hypotensive; analgesic; cytostatic; antiasthmatic; osteopathic;		
KW	cardiovascular; antiulcer; nootropic; anticonvulsant; antiallergic;		
KW	neuroleptic; antidote; antiparkinsonian; neuroprotective; gene therapy;		
KW	antidepressant; antiasthmatic; diuretic; chromosome 11q12.2; ds.		
XX			
OS	Homo sapiens.		
XX			
FF	Key	Location/Qualifiers	
FT	misc_feature	394..1689	
FT		/*tag= a	
FT		/note= "Human NPY-like GPCR gene sequence (ABK14956)"	
XX			
PN	W0200204518-A2.		
XX			
PD	17-JAN-2002.		
XX			
PF	06-JUL-2001; 2001WO-US21276.		
XX			
PR	06-JUL-2000; 2000US-216523P.		
XX			
PA	(FARB) BAYER CORP.		
XX			
PI	Bloomquist BT, Zhelnin L;		
XX			
DR	WPI; 2002-148166/19.		
XX			
PT	New neuropeptide Y-like G protein-coupled receptor, for detecting		
PT	regulators for preventing, ameliorating, or correcting e.g. obesity,		
PT	anorexia, diabetes, hypotension, hypertension, pain, cancers, or		
PT	neurological disorders -		
XX			
PS	Disclosure; Page 90; 91pp; English.		
XX			
CC	The present invention relates to a new polynucleotide encoding a		
CC	polypeptide neuropeptide Y-like G protein-coupled receptor (NPY-like		
CC	GPCR), comprising a 431 amino acid sequence, given in the specification.		
CC	The polynucleotide of the invention is used to produce a NPY-like GPCR		
CC	polypeptide. The complement of the polynucleotide can be used to detect		
CC	a coding sequence for a NPY-like GPCR. A reagent, preferably an antibody,		
CC	that binds to NPY-like GPCR can be used to detect it. The NPY-like GPCR		
CC	can be used to screen for agents that can regulate the activity of it. A		
CC	reagent that binds to or regulates NPY-like GPCR can be used to reduce		
CC	the biological activity of NPY-like GPCR, or treat a disorder associated		
CC	with abnormal expression of NPY-like GPCR. The reagent is useful for		
CC	preventing, ameliorating or correcting dysfunctions or diseases such as		
CC	obesity, anorexia, bulimia, diabetes, hypotension, hypertension, cocaine		
CC	withdrawal, pain, cancers, asthma, urinary retention, osteoporosis,		
CC	angina pectoris, myocardial infarction, ulcers, allergies, congestive		

CC heart failure, memory enhancement, cardiac and cerebral vasospasm,
CC pheochromocytoma, ganglioneuroblastoma, Huntington's disease, severe
CC mental retardation, Alzheimer's disease, Parkinson's disease, psychotic
CC and neurological disorders including anxiety, schizophrenia, manic
CC depression, delirium, dementia and dyskinesias. The polypeptide may also
CC be used in raising specific antibodies. The present nucleic acid sequence
CC contains the human NYP-like GPCR gene (ABK14956) located on chromosome
XX 11q12.2.

Query Match 69.1%; Score 1668.4; DB 24; Length 1710;
Best Local Similarity 99.9%; Pred. No. 5.1e-255;
Matches 1669; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 GCCAGAGCGCCAGGACCTAGCGTGGCGCTCCAGACCCAGACCGTGGCGGCCCTCG 60
41 GCCAGAGCGCCAGGACCTCGCGTGGCGCTCCAGACCCAGACCGTGGCGGCCCTCG 100
61 CTTAGGGAAGAGCAAGGGAAGAACTTTATTGGAACCGCAACATTTTGGTCACTGAG 120
101 CTTAGGGAAGAGCAAGGGAAGAACTTTATTGGAACCGCAACATTTTGGTCACTGAG 160
121 ATCGAGTCTCCAGTCTTTGGCTTCGGCTTCCTTTATCGTGGGTTTATCCCTGAGCTG 180
161 ATCGAGTCTCCAGTCTTTGGCTTCGGCTTCCTTTATCGTGGGTTTATCCCTGAGCTG 220
181 CTCTCTCTTCCGAACTCCCGGGGTGACGCTAGAGCCCTCCCGCGGGTGACTCCAG 240
221 CTCTCTTTCGGAACCTCCCGGGGTGACGCTAGAGCCCTCCCGCGGGTGACTCCAG 280
241 AGTAGAGGAAGGAGCGGCTTCGGCTGGTCCCGGAAGCCCTCGCTGCCCGCAGATG 300
281 AGTAGAGGAAGGAGCGGCTTCGGCTGGTCCCGGAAGCCCTCGCTGCCCGCAGATG 340
301 CGGATGGCCAGCAGTACGGCGGTGGCCCGCTCCCGGGAGCGCAGCAATGCGAGG 360
341 CGGATGGCCAGCAGTACGGCGGTGGCCCGCTCCCGGGAGCGCAGCAATGCGAGG 400
361 CGCTTAAACATTACCCCGGAGCAGTCTCTCGGCTGTGCGGACCAACACCTGAGCGGG 420
401 CGCTTAAACATTACCCCGGAGCAGTCTCTCGGCTGTGCGGACCAACACCTGAGCGGG 460
421 AGCAGTTATCGCTCTGTACCGGCTGCGACCGCTCGTTACACCCAGAGCTGCCGGAC 480
461 AGCAGTTATCGCTCTGTACCGGCTGCGACCGCTCGTTACACCCAGAGCTGCCGGAC 520
481 GCGCCAGCTGSCCTCTGCTCAGCGGCTGCTCATCTTCGCCCTGGCGCTTTGGCA 540
521 GCGCCAGCTGSCCTCTGCTCAGCGGCTGCTCATCTTCGCCCTGGCGCTTTGGCA 580
541 ATGCTCTGGTGTCTACGTGTGAGCCGCGCAGCAAGCCATGCGCACCTGACCAACATCT 600
581 ATGCTCTGGTGTCTACGTGTGAGCCGCGCAGCAAGCCATGCGCACCTGACCAACATCT 640
601 TTATCTGCTCTTGGCGCTCAGTACCTGCTCATACCTTTCTTGCAATTCGCCGTCACA 660
641 TTATCTGCTCTTGGCGCTCAGTACCTGCTCATACCTTTCTTCTGCAATTCGCCGTCACA 700
661 TGCTCCAGAACATTTCCGACACTGCTGGGGGTGCTTTTCATTTGCAAGATGGTGCAT 720
701 TGCTCCAGAACATTTCCGACACTGCTGGGGGTGCTTTTCATTTGCAAGATGGTGCAT 760
721 TTGTCAGTCTACCGTGTGTGACAGAAATCCTCACTATGACCTGCAATGCTGTGGAAA 780
761 TTGTCAGTCTACCGTGTGTGACAGAAATCCTCACTATGACCTGCAATGCTGTGGAAA 820
781 GGCACAGGGAATTTGTCATCTTTTAAATGAAGTGCGCAATACCAACCGAAGGGTT 840
821 GGCACAGGGAATTTGTCATCTTTTAAATGAAGTGCGCAATACCAACCGAAGGGTT 880
841 TCACATGCTAGTGTGCTGGCTGGTGGGAGTCACTGCTAGGATCACCATGTCGACG 900

Db 881 TCAATGCTAGTGTGTGTGCTGGTGGCAGTCATGCTAGGATCACCCATGTGGCAG 940
Qy 901 TGCAACAACTTGAGATCAATATGACATTCCTATATGAAAAGAAACACATCTGCTGCTTAG 960
Db 941 TGCAACAACTTGAGATCAATATGACATTCCTATATGAAAAGAAACACATCTGCTGCTTAG 1000
Qy 961 AAGAGTGGACCAAGCCCTGTGCACCAAGAGATCTACACACCTTCATCTCTCATCTCT 1020
Db 1001 AAGAGTGGACCAAGCCCTGTGCACCAAGAGATCTACACACCTTCATCTCTCATCTCT 1060
Qy 1021 TCCTCTGCTCTTATGCTGATGCTTATCTGTCAGTAAATTTGGTATGAACCTTTGGA 1080
Db 1061 TCCTCTGCTCTTATGCTGATGCTTATCTGTCAGTAAATTTGGTATGAACCTTTGGA 1120
Qy 1081 TAAAGAAAAGAGTTGGGATGGTTCAGTCTCGAATCTTTCATGTAAGAAAAGAAATGTCCA 1140
Db 1121 TAAAGAAAAGAGTTGGGATGGTTCAGTCTCGAATCTTTCATGTAAGAAAAGAAATGTCCA 1180
Qy 1141 AAATAGCCAGGAAGAAAACGAGCTGCTATTATGATGGTGACAGTGGTCTCTCTTTG 1200
Db 1181 AAATAGCCAGGAAGAAAACGAGCTGCTATTATGATGGTGACAGTGGTCTCTCTTTG 1240
Qy 1201 CTGTGCTGGGACCAATTCATGTTTCCATATGATGATGATGATGATGATGATGATGATG 1260
Db 1241 CTGTGCTGGGACCAATTCATGTTTCCATATGATGATGATGATGATGATGATGATGATG 1300
Qy 1261 AGGAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1320
Db 1301 AGGAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1360
Qy 1321 CCACCTCATCTGTAATCCCAATTCATGCTATGATGATGATGATGATGATGATGATGATG 1380
Db 1361 CCACCTCATCTGTAATCCCAATTCATGCTATGATGATGATGATGATGATGATGATGATG 1420
Qy 1381 TTTTGTCTGCGATTTGTTTATGCTAGTAAATGAACTTCTCTCCAGCACAAGGCGATG 1440
Db 1421 TTTTGTCTGCGATTTGTTTATGCTAGTAAATGAACTTCTCTCCAGCACAAGGCGATG 1480
Qy 1441 GAAATTCAGGAATTAACATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1500
Db 1481 GAAATTCAGGAATTAACATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1540
Qy 1501 TGGAGGAAACCAAGGAGAGCAATTCAGTATGATGATGATGATGATGATGATGATGATGATG 1560
Db 1541 TGGAGGAAACCAAGGAGAGCAATTCAGTATGATGATGATGATGATGATGATGATGATGATG 1600
Qy 1561 AGCAGAGGAG 1620
Db 1601 AGCAGAGGAG 1660
Qy 1621 AGAATTCCTCTTACAGAGTGGGCAATTAATTAACAATATCTTTCATAAT 1670
Db 1661 AGAATTCCTCTTACAGAGTGGGCAATTAATTAACAATATCTTTCATAAT 1710

RESULT 5
AAH49502

ID AAH49502 standard; DNA; 1296 Bp.

XX AC AAH49502;

XX XX 21-SEP-2001 (first entry)

XX Human GTP-binding protein-coupled receptor GPRv11 coding sequence.

DE DE GTP-binding protein-coupled receptor; neuroprotective; immunomodulatory;
KW muscular; urinary; circulatory; anorectic; gene therapy; human;
KW guanidine triphosphate; G-protein; ds.

OS Homo sapiens.

XX PN WO200148189-A1.

XX

PD 05-JUL-2001.
 XX
 PF 28-DEC-2000; 2000WO-UP09409.
 XX
 PR 28-DEC-1999; 99JP-0375152.
 PR 31-MAR-2000; 2000JP-0101339.
 PR 23-MAY-2000; 2000JP-0155978.
 XX
 PA (HELI-) HELIX RES INST.
 XX
 PI Matsumoto S, Oda T, Saito Y, Morikawa N, Yoshida K, Suwa M;
 PI Sugiyama T;
 XX
 DR WPI; 2001-425663/45.
 DR P-PSDB; AAG64289.
 XX
 PT Family of guanosine triphosphate binding protein coupled receptors and
 PT genes encoding them for treatment and prevention of diseases associated
 PT with these receptors -
 XX
 PS Claim 1; Pages 82-83; 137pp; Japanese.
 CC The present sequence is the coding sequence for a human guanosine
 CC triphosphate (GTP)-binding protein-coupled receptor. The receptor is
 CC useful for the investigation, diagnosis, treatment and prevention of
 CC diseases associated with GTP-binding protein-coupled receptors, including
 CC neurological, circulatory, digestive system, immune system, muscle and
 CC urinary system disorders. GTP-binding proteins are also known as
 CC G-proteins.
 XX
 SQ Sequence 1296 BP; 344 A; 305 C; 301 G; 346 T; 0 other;
 Query Match 53.7%; Score 1296; DB 22; Length 1296;
 Best Local Similarity 100.0%; Pred. No. 3.6e-196;
 Matches 1296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 354 ATGCGAGGCGCTTAACATTAACCGCGGAGCAGTCTCTCGGCTGCGGGACACACCTG 413
 DB 1 ATGCGAGGCGCTTAACATTAACCGCGGAGCAGTCTCTCGGCTGCGGGACACACCTG 60
 QY 414 ACGCGGGAGCAGTTCATCGCTCTGTACCGGCTGCGAGCGCTCGTCTACACCCACGAGCTG 473
 DB 61 ACGCGGGAGCAGTTCATCGCTCTGTACCGGCTGCGAGCGCTCGTCTACACCCACGAGCTG 120
 QY 474 CCGGGAQCGCGCAAGTGGCCCTCGTGTCAQCGGCTGCTCATCTTCGCCCTGGCGCTC 533
 DB 121 CCGGGAQCGCGCAAGTGGCCCTCGTGTCAQCGGCTGCTCATCTTCGCCCTGGCGCTC 180
 QY 534 TTTGGCAATGCTCTGGTGTCTACGTGTGACCCCGCAGCAAGCCATGCGCACCGTCACC 593
 DB 181 TTTGGCAATGCTCTGGTGTCTACGTGTGACCCCGCAGCAAGCCATGCGCACCGTCACC 240
 QY 594 AACATCTTTATCTGCTCCCTGGCGCTCACTGACCTGCTCATCACTTCTTCGTGCAATCC 653
 DB 241 AACATCTTTATCTGCTCCCTGGCGCTCACTGACCTGCTCATCACTTCTTCGTGCAATCC 300
 QY 654 GTCAACATGCTCCAGAACATTTCCGCAACTGCTGGGGGGTCTTTCATTTGCAAGATG 713
 DB 301 GTCAACATGCTCCAGAACATTTCCGCAACTGCTGGGGGGTCTTTCATTTGCAAGATG 360
 QY 714 GTGGCAATTTGCTCACTCTACCGCTGTGTGACAGAAATCCTCACTATGACCTGCAATGCT 773
 DB 361 GTGGCAATTTGCTCACTCTACCGCTGTGTGACAGAAATCCTCACTATGACCTGCAATGCT 420
 QY 774 GTGGAAAGGCACACAGGCACTTGTGCATCCCTTTAAATGAAGTGGCAATACACCAACCGA 833
 DB 421 GTGGAAAGGCACACAGGCACTTGTGCATCCCTTTAAATGAAGTGGCAATACACCAACCGA 480
 QY 834 AGGGCTTTTCAATGCTAGGTGTGGTCTGGCTGGTGGAGTCACTGATGATCAACCCATG 893
 DB 481 AGGGCTTTTCAATGCTAGGTGTGGTCTGGCTGGTGGAGTCACTGATGATCAACCCATG 540
 QY 894 TGGCAGCTGCACAACTTGAGATCAAAATATGACTTCCTATATGAAAGGAACACATCTGC 953

DB 541 TGGCAGCTGCACAACTTGAGATCAAAATATGACTTCCTATATGAAAGGAACACATCTGC 600
 QY 954 TGCTTAGAAGAGTGGACACAGCCCTGTGACACAGAGATCTACACACCTTCATCTTGTCTC 1013
 DB 601 TGCTTAGAAGAGTGGACACAGCCCTGTGACACAGAGATCTACACACCTTCATCTTGTCTC 660
 QY 1014 ATCTCTTCTCTCCCTGCTCTTATGATGCTTATCTGTACAGTAAATTTGGTTATGAA 1073
 DB 661 ATCTCTTCTCTCCCTGCTCTTATGATGCTTATCTGTACAGTAAATTTGGTTATGAA 720
 QY 1074 CTTTGGATAAAGAAAAGAGTTGGGATGTTTCAGTGTTCGAACTATTCATGGAAAAGAA 1133
 DB 721 CTTTGGATAAAGAAAAGAGTTGGGATGTTTCAGTGTTCGAACTATTCATGGAAAAGAA 780
 QY 1134 ATGTCCAAAATAGCCAGGAAGAAAGACAGCTGTCAATATGATGGTGCACAGTGGTGCCT 1193
 DB 781 ATGTCCAAAATAGCCAGGAAGAAAGACAGCTGTCAATATGATGGTGCACAGTGGTGCCT 840
 QY 1194 CTCCTTTGCTGTGCTGGGCACCACTTCATGCTGTGCCATATGATGATTAATACAGTAAT 1253
 DB 841 CTCCTTTGCTGTGCTGGGCACCACTTCATGCTGTGCCATATGATGATTAATACAGTAAT 900
 QY 1254 TTTGAAAAGGAATATGATGATGTCAATCAAGATGATTTTGTCTATCGTCAAAATTAAT 1313
 DB 901 TTTGAAAAGGAATATGATGATGTCAATCAAGATGATTTTGTCTATCGTCAAAATTAAT 960
 QY 1314 GGAATTTTCCAACTCCATCTGTAATCCCATCTCTATGCAATTTATGAATGAAGAACTTCAA 1373
 DB 961 GGAATTTTCCAACTCCATCTGTAATCCCATCTCTATGCAATTTATGAATGAAGAACTTCAA 1020
 QY 1374 AAAAATGTTTTGTCTGCAGTTTGTATTGTCATAGTAATAAACCCTTCTCTCCAGCAAA 1433
 DB 1021 AAAAATGTTTTGTCTGCAGTTTGTATTGTCATAGTAATAAACCCTTCTCTCCAGCAAA 1080
 QY 1434 AGGCAATGGAATTCAGGAATTCAGTAATGATGCGGAAGAAAGCAAGTTTTTCCCTCAGAG 1493
 DB 1081 AGGCAATGGAATTCAGGAATTCAGTAATGATGCGGAAGAAAGCAAGTTTTTCCCTCAGAG 1140
 QY 1494 AATCCAGTGGAGGAAACCCAAAGGAGAGCAATTCAGTGTATGCAACATGGAAGTCAAAATG 1553
 DB 1141 AATCCAGTGGAGGAAACCCAAAGGAGAGCAATTCAGTGTATGCAACATGGAAGTCAAAATG 1200
 QY 1554 TGTGAACAGACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1613
 DB 1201 TGTGAACAGACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1260
 QY 1614 CTGGCTGAGAAATTCCTCTTTAGACAGTGGGCAATTA 1649
 DB 1261 CTGGCTGAGAAATTCCTCTTTAGACAGTGGGCAATTA 1296

RESULT 6
 AAC87690
 ID AAC87690 standard; DNA; 1296 BP.
 XX
 AC AAC87690;
 XX
 DT 27-MAR-2001 (first entry)
 XX
 DE Human G protein-coupled receptor AXOR16 DNA.
 KW
 KW AXOR16; human; G protein-coupled receptor; 7TM receptor;
 KW chromosome 11q12.2; infection; viral; bacterial; fungal;
 KW protozoan; HIV-1; HIV-2; pain; cancer; diabetes; obesity;
 KW anorexia; bulimia; osteoporosis; asthma; allergy; urinary retention;
 KW acute heart failure; hypotension; hypertension; angina pectoris;
 KW myocardial infarction; stroke; ulcer; migraine; vomiting;
 KW psychotic disorder; neurological disorder; anxiety; schizophrenia;
 KW manic depression; bipolar disorder; depression; delirium; dementia;
 KW severe mental retardation; dyskinesia; Parkinson's disease;
 KW Huntington's disease; Gilles de la Tourette's syndrome; gene therapy;
 KW vaccine; drug screening; signal transduction; ds.

XX OS Homo sapiens.
 XX PN WO200078809-A1.
 XX PD 28-DEC-2000.
 XX PF 19-JUN-2000; 2000WO-US16869.
 XX PR 21-JUN-1999; 99US-0337105.
 XX PA (SMIX) SMITHKLINE BEECHAM CORP.
 XX PI Elshourbagy N, Shabon U;
 XX WPI; 2001-102699/11.
 XX DR P-SDB; AAB48963.
 XX PT New AXOR16, a G-protein coupled receptor polypeptide for screening
 XX PT agonists and antagonists and for diagnosing and treating microbial
 XX PT infections, cancer, neurological disorders and asthma -
 XX PS Claim 2; Page 29; 31pp; English.
 XX CC The invention relates to the human G protein-coupled receptor AXOR16
 CC (AAB48963) to DNA encoding AXOR16 (AAC87690), and to AXOR16 fragments
 CC and variants. Like all G protein-coupled receptors, AXOR16 has 7
 CC putative transmembrane domains and is involved in signal transduction.
 CC AXOR16 has homology with Gadus morhua neuropeptide (NPVFB) F and
 CC homology/ structural similarity with Danio rerio neuropeptide Y (NPYRYA).
 CC The human AXOR16 gene is located on chromosome 11q12.2. The invention
 CC also relates to expression vectors and host cells comprising AXOR16 DNA,
 CC to recombinant expression of AXOR16, and to an AXOR16-specific antibody.
 CC AXOR16 proteins and nucleotides may be used to treat a wide variety of
 CC disorders including bacterial, fungal, protozoal and viral infections,
 CC particularly HIV-1 or HIV-2 infections, pain; cancers; benign prostatic
 CC hypertrophy; diabetes; obesity; anorexia; bulimia; osteoporosis; asthma;
 CC allergies; urinary retention; acute heart failure; hypotension;
 CC hypertension; angina pectoris; myocardial infarction; stroke; ulcers;
 CC migraine; vomiting; psychotic and neurological disorders such as
 CC anxiety, schizophrenia, manic depression, depression, delirium, dementia,
 CC and severe mental retardation, and dyskinesias, such as Parkinson's
 CC disease, Huntington's disease or Gilles de la Tourette's syndrome.
 CC AXOR16 proteins, and nucleotides are useful as vaccines, and AXOR16
 CC proteins, nucleotides and antibodies may be used in screening compounds
 CC for their ability to modulate AXOR16 activity or expression. AXOR16
 CC proteins are also useful for inducing an immunological response in a
 CC mammal against the above diseases, for antibody production, and to
 CC identify membrane bound or soluble receptors for AXOR16. AXOR16
 CC nucleotides are also useful as diagnostic reagents and in chromosome
 CC localisation and tissue expression studies. The present sequence
 CC represents DNA encoding human AXOR16.
 XX SQ Sequence 1296 BP; 344 A; 305 C; 301 G; 346 T; 0 other;

Query Match 53.7%; Score 1296; DB 22; Length 1296;
 Best Local Similarity 100.0%; Pred. No. 3.6e-196;
 Matches 1296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 354 ATCCAGCGCTTAACATTACCCGGAGCAGTTCTCTCGGCTGTCGGGACCAACCTG 413
 DB 1 ATCCAGCGCTTAACATTACCCGGAGCAGTTCTCTCGGCTGTCGGGACCAACCTG 60
 QY 414 ACSCGGGAGCAGTTTCATCGCTCTGTACCGGCTGCGACCGCTCTACACCCAGAGCTG 473
 DB 61 ACSCGGGAGCAGTTTCATCGCTCTGTACCGGCTGCGACCGCTCTACACCCAGAGCTG 120
 QY 474 CCGGGACGCGCCCAAGCTGGCCCTCTGTGCTCACCGGGTGTCTATCTTCGCCCTTGGGCTC 533
 DB 121 CCGGGACGCGCCCAAGCTGGCCCTCTGTGCTCACCGGGTGTCTATCTTCGCCCTTGGGCTC 180
 QY 534 TTTCGCAATGCTCTGGTGTCTACGTGGTCAACCGGACGAGGCCATCGCCACCGTCAAC 593

DB 181 TTTCGCAATGCTCTGGTGTCTACGTGGTGAACCCGACGCAAGGCCATGCGCACCGTCAAC 240
 QY 594 AACATCTTTATCTGCTCCCTTGGCGCTCAGTGACCTGCTCATCACCTTCTTCTGCAATCCC 653
 DB 241 AACATCTTTATCTGCTCCCTTGGCGCTCAGTGACCTGCTCATCACCTTCTTCTGCAATCCC 300
 QY 654 GTCACCATGCTCCAGAAACATTTCCGACAACTGGCTGGGGGTGCTTTTCATTTTCAAGATG 713
 DB 301 GTCACCATGCTCCAGAAACATTTCCGACAACTGGCTGGGGGTGCTTTTCATTTTCAAGATG 360
 QY 714 GTGCCATTTGTCAAGTCTACCGCTGTGTGTGACAGAAATCCTCACTATGACCTGCAATGCT 773
 DB 361 GTGCCATTTGTCAAGTCTACCGCTGTGTGTGACAGAAATCCTCACTATGACCTGCAATGCT 420
 QY 774 GTGGAAGGCACCCAGGCACTTTGTGCATCTTTTAAATGAAGTGCCAAATACACCAACCGA 833
 DB 421 GTGGAAGGCACCCAGGCACTTTGTGCATCTTTTAAATGAAGTGCCAAATACACCAACCGA 480
 QY 834 AGGGCTTTTCACAATGCTAGT 893
 DB 481 AGGGCTTTTCACAATGCTAGT 540
 QY 894 TGGCAGCTGCAACAACTTGAGATCAAAATGATCTTCTATATGAAAAGGAAACATCTGTC 953
 DB 541 TGGCAGCTGCAACAACTTGAGATCAAAATGATCTTCTATATGAAAAGGAAACATCTGTC 600
 QY 954 TGCTTAGAAGAGTGGACCAAGCTGTGACCAAGAGATCTACACCACTTTCATCTTGTGTC 1013
 DB 601 TGCTTAGAAGAGTGGACCAAGCTGTGACCAAGAGATCTACACCACTTTCATCTTGTGTC 660
 QY 1014 ATCTCTTCTCTCTGCTCTTATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1073
 DB 661 ATCTCTTCTCTCTGCTCTTATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 720
 QY 1074 CTTTGCATTAAGAAAGAGTGTGGGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1133
 DB 721 CTTTGCATTAAGAAAGAGTGTGGGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 780
 QY 1134 ATGTCCAAATAGCCAGGAAGAAAGAGCTGTCTATATGATGTGTGTGTGTGTGTGTGTGT 1193
 DB 781 ATGTCCAAATAGCCAGGAAGAAAGAGCTGTCTATGTGTGTGTGTGTGTGTGTGTGTGTGT 840
 QY 1194 CTCTTTGCTGT 1253
 DB 841 CTCTTTGCTGT 900
 QY 1254 TTTGAAAAGGAATATGATGATGTCAATCAAGATGATTTTGTCTATCGTGCAAAATATT 1313
 DB 901 TTTGAAAAGGAATATGATGATGTCAATCAAGATGATTTTGTCTATCGTGCAAAATATT 960
 QY 1314 GGATTTTCCAACTCCATCTGTATCCCATTTGTCTATGTGTGTGTGTGTGTGTGTGTGTGT 1373
 DB 961 GGATTTTCCAACTCCATCTGTATCCCATTTGTCTATGTGTGTGTGTGTGTGTGTGTGTGT 1020
 QY 1374 AAAAATGTTTTGT 1433
 DB 1021 AAAAATGTTTTGT 1080
 QY 1434 AGGCATGGAATTCAGGATTAATGATGCGGAGAAAGCAAGTTCCTTCCCTCAGAGAG 1493
 DB 1081 AGGCATGGAATTCAGGATTAATGATGCGGAGAAAGCAAGTTCCTTCCCTCAGAGAG 1140
 QY 1494 AATCCAGTGGAGAAACCAAAGGAAGCATTCAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1553
 DB 1141 AATCCAGTGGAGAAACCAAAGGAAGCATTCAGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1200
 QY 1554 TGTGAACAGACAG 1613
 DB 1201 TGTGAACAGACAG 1260
 QY 1614 CTGGCTGAGAATCTCTCTTTAGACAGTGGGCAATTAA 1649
 DB 1261 CTGGCTGAGAATCTCTCTTTAGACAGTGGGCAATTAA 1296

RESULT 7
 ABK86287
 ID ABK86287 standard; cDNA; 1296 BP.
 XX AC ABK86287;
 XX DT 27-AUG-2002 (first entry)
 XX DE Human TGR346 cDNA.
 XX KW Human; TGR346; gene; ss; G-protein coupled receptor; GPCR; TGR;
 KW TGR-associated disorder; signal transduction; renal failure; nephritis;
 KW hypothyroidism; hypogonadism; retinitis pigmentosa; growth disorder;
 KW diabetes insipidus; hyperprolactinaemia; thirst disturbance; appetite;
 KW sleep disturbance; temperature regulation; blood pressure; hypothalamus;
 KW circadian rhythm.
 XX OS Homo sapiens.
 XX FH Key Location/Qualifiers
 XX FT 1..1296
 XX FT CDS /tag= a
 XX FT /product= "Human TGR346 protein"
 XX PN WO200242458-A2.
 XX PD 30-MAY-2002.
 XX PF 21-NOV-2001; 2001WO-US43404.
 XX PR 22-NOV-2000; 2000US-252841P.
 XX PR 22-DEC-2000; 2000US-257636P.
 XX PR 12-JAN-2001; 2001US-261379P.
 XX PR 28-MAR-2001; 2001US-279554P.
 XX PR 29-MAR-2001; 2001US-280896P.
 XX PA (TULA-) TULARIK INC.
 XX PI Tian H, Zhao J, Chen J, Cutler G, An S, Dai K, Gupta JS;
 XX WPI; 2002-463633/49.
 XX DR P-PSDB; AAU97735.
 XX PT New isolated G-protein coupled receptor polypeptide, termed TGR, for
 PT diagnosis and treatment of diseases such as renal failure, nephritis,
 PT hypothyroidism, diabetes insipidus, and disturbances of thirst and
 PT sleep.
 XX PS Claim 42; Page 74; 98pp; English.
 XX CC The invention relates to a G-protein coupled receptor polypeptide (GPCR),
 CC termed TGR, and its associated nucleic acid. The sequences of the
 CC invention are useful for identifying a compound that modulates signal
 CC transduction and for identifying a mammal having a TGR-associated
 CC disorder. The proteins and nucleic acids are useful in diagnosis and
 CC treatment of diseases or conditions such as renal failure, nephritis,
 CC hypothyroidism, hypogonadism, retinitis pigmentosa, growth disorders,
 CC diabetes insipidus, hyperprolactinaemia and disturbances of thirst,
 CC sleep, temperature regulation, appetite, blood pressure or any other
 CC syndrome or disease associated with the hypothalamus. The sequences can
 CC be used in regulation of circadian rhythms, for use as genetic markers
 CC for the identification of mutations associated with diseases resulting
 CC from GPCR inactivation in particular cell types and for identification of
 CC modulators of GPCR signal transduction. This sequence represents cDNA
 CC encoding the human TGR346 polypeptide.
 XX SQ Sequence 1296 BP; 344 A; 305 C; 301 G; 346 T; 0 other;
 Query Match 53.7%; Score 1296; DB 24; Length 1296;
 Best Local Similarity 100.0%; Pred. No. 3.6e-136;
 Matches 1296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 354 ATGCGAGGCTTAACATTACCCGGAGCAGTTCTCTCGGCTGCTGGGGACCAACCTG 413
 Db 1 ATGCGAGGCTTAACATTACCCGGAGCAGTTCTCTCGGCTGCTGGGGACCAACCTG 60
 QY 414 ACGCGGAGCAGTTTCATCGCTCTGTACCGGCTGGAGCGGCTCGTCTACACCCAGAGCTG 473
 Db 61 ACGCGGAGCAGTTTCATCGCTCTGTACCGGCTGGAGCGGCTCGTCTACACCCAGAGCTG 120
 QY 474 CCGGACGCGCCAAAGCTGGCCCTCGTCTCAACCGGCTGTCTCATCTTGGCCCTGGCGCTC 533
 Db 121 CCGGACGCGCCAAAGCTGGCCCTCGTCTCAACCGGCTGTCTCATCTTGGCCCTGGCGCTC 180
 QY 534 TTTCGCAATGCTCTGGGTTCTACGTGTGACCCGCGCAGGCGCATGCCACCGTCAAC 593
 Db 181 TTTCGCAATGCTCTGGGTTCTACGTGTGACCCGCGCAGGCGCATGCCACCGTCAAC 240
 QY 594 AACATCTTTATCTGCTCTCTGGGCTCAGTGACCTGCTCATCTTCTTCTGCAATCCC 653
 Db 241 AACATCTTTATCTGCTCTCTGGGCTCAGTGACCTGCTCATCTTCTTCTGCAATCCC 300
 QY 654 GTACCAATGCTCCAGAACATTTCCGACAACTGGCTGGGGGTGCTTTTCATTTGCAAGATG 713
 Db 301 GTACCAATGCTCCAGAACATTTCCGACAACTGGCTGGGGGTGCTTTTCATTTGCAAGATG 360
 QY 714 GTGCCATTTGTCCAGTCTACCGCTGTTGTGACAGAAATCCTCACTATGACCTGCAATGCT 773
 Db 361 GTGCCATTTGTCCAGTCTACCGCTGTTGTGACAGAAATCCTCACTATGACCTGCAATGCT 420
 QY 774 GTGAAAGGCCACAGGCACTTGTGCAATCTTTTAAATGAAGTGGCAATACACCAACCGA 833
 Db 421 GTGAAAGGCCACAGGCACTTGTGCAATCTTTTAAATGAAGTGGCAATACACCAACCGA 480
 QY 834 AGGCTTTTCACATGCTAGTGTGCTGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 893
 Db 481 AGGCTTTTCACATGCTAGTGTGCTGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 540
 QY 894 TGGCAGCTGCAACAACTTGAGATCAAAATATGACTTCTATATGAAAAAGGAACACATGCTG 953
 Db 541 TGGCAGCTGCAACAACTTGAGATCAAAATATGACTTCTATATGAAAAAGGAACACATGCTG 600
 QY 954 TGCTTAGAGAGTGGACAGCCCTGTGCCACAGAGATCTACACCACTTCATCTTGTGTC 1013
 Db 601 TGCTTAGAGAGTGGACAGCCCTGTGCCACAGAGATCTACACCACTTCATCTTGTGTC 660
 QY 1014 ATCTCTTCT 1073
 Db 661 ATCTCTTCT 720
 QY 1074 CTTTGGATAAAGAAAAGAGTTGGGGATGGTTCACTGCTTCGAATCTTTCATGGAAGAA 1133
 Db 721 CTTTGGATAAAGAAAAGAGTTGGGGATGGTTCACTGCTTCGAATCTTTCATGGAAGAA 780
 QY 1134 ATGTCCAAAATAGCCAGAGAAAGAAACGAGCTGTCTATATGATGGTGACAGTGGTGGCT 1193
 Db 781 ATGTCCAAAATAGCCAGAGAAAGAAACGAGCTGTCTATATGATGGTGACAGTGGTGGCT 840
 QY 1194 CTCTTCT 1253
 Db 841 CTCTTCT 900
 QY 1254 TTTGAAAAGAAATATGATGATGTCCAAATCAAGATGATTTTGGTCTATGCTGCAATATTT 1313
 Db 901 TTTGAAAAGAAATATGATGATGTCCAAATCAAGATGATTTTGGTCTATGCTGCAATATTT 960
 QY 1314 GGATTTTCCAACTCCAFCTCTGAATCCCAATCTCTATGCAATTTATGAATGAAATCTCAA 1373
 Db 961 GGATTTTCCAACTCCAFCTCTGAATCCCAATCTCTATGCAATTTATGAATGAAATCTCAA 1020
 QY 1374 AAAAAATGTTTGTCTGAGTTTGTATTGATAGTAAATAAAACCTTCTCTCCAGCAAA 1433
 Db 1021 AAAAAATGTTTGTCTGAGTTTGTATTGATAGTAAATAAAACCTTCTCTCCAGCAAA 1080

QY 1434 AGGCATGGAATTCAGGAATACATGATGCGGAGAAAGCAAGTTTCCCTCAGAGAG 1493
 |||||
 Db 1081 AGGCATGGAATTCAGGAATACATGATGCGGAGAAAGCAAGTTTCCCTCAGAGAG 1140
 |||||
 QY 1494 AATCCAGTGGAGGAAACCAAGGAGAACATTCAGTGATGCAACATGGAAGTCAAAATG 1553
 |||||
 Db 1141 AATCCAGTGGAGGAAACCAAGGAGAACATTCAGTGATGCAACATGGAAGTCAAAATG 1200
 |||||
 QY 1554 TGTGAACACAGACAGAGGAGAAAGGCTCAAAACGACATCTTGCTCTCTTTAGTGTCTGAA 1613
 |||||
 Db 1201 TGTGAACACAGACAGAGGAGAAAGGCTCAAAACGACATCTTGCTCTCTTTAGTGTCTGAA 1260
 |||||
 QY 1614 CTGGCTGAGAAATTCCTTTTACAGAGTGGGATTA 1649
 |||||
 Db 1261 CTGGCTGAGAAATTCCTTTTACAGAGTGGGATTA 1296
 |||||

RESULT 8

ABK14956

ID ABK14956 standard; DNA; 1296 BP.

XX AC

XX ABK14956;

XX DT

XX 08-MAY-2002 (first entry)

XX DE

XX Human neuropeptide Y-like GPCR (NPY-like GPCR) gene sequence.

XX KW

XX NPY-like GPCR; anorectic; antidiabetic; tranquilizer; hypertensive; gene;

XX KW

XX hypotensive; analgesic; cytosolic; antispasmodic; osteopathic;

XX KW

XX cardiovascular; antitumor; neurotropic; anticonvulsant; antiallergic;

XX KW

XX neuroleptic; antidote; antiparkinsonian; neuroprotective; gene therapy;

XX KW

XX antidepressant; antispasmodic; diuretic; chromosome 11q12.2; ds.

XX OS

XX Homo sapiens.

XX PH

XX Key Location/Qualifiers

XX CDS

XX 1..1296

XX /*tag= a

XX /product= "Human NPY-like GPCR protein"

XX PN

XX WO200204518-A2.

XX PD

XX 17-JAN-2002.

XX PF

XX 06-JUL-2001; 2001WO-US21276.

XX PR

XX 06-JUL-2000; 2000US-216523P.

XX XX

XX (FARB) BAYER CORP.

XX PA

XX Bloomquist BT, Zhelnin L;

XX PI

XX WPI; 2002-148166/19.

XX DR

XX P-PSDB; ABU76035.

XX XX

XX New neuropeptide Y-like G protein-coupled receptor, for detecting

XX PT

XX regulators for preventing, ameliorating, or correcting e.g. obesity,

XX PT

XX anorexia, diabetes, hypotension, hypertension, pain, cancers, or

XX PT

XX neurological disorders

XX XX

XX Claim 2; Fig 1; 9lpp; English.

XX PS

XX The present invention relates to a new polynucleotide encoding a

XX CC

XX polypeptide neuropeptide Y-like G protein-coupled receptor (NPY-like

XX CC

XX GPCR) comprising a 431 amino acid sequence, given in the specification.

XX CC

XX The polynucleotide of the invention is used to produce a NPY-like GPCR

XX CC

XX polypeptide. The complement of the polynucleotide can be used to detect

CC with abnormal expression of NPY-like GPCR. The reagent is useful for
 CC preventing, ameliorating or correcting dysfunctions or diseases such as
 CC obesity, anorexia, bulimia, diabetes, hypotension, hypertension, cocaine
 CC withdrawal, pain, cancers, asthma, urinary retention, osteoporosis,
 CC angina pectoris, myocardial infarction, ulcers, allergies, congestive
 CC heart failure, memory enhancement, cardiac and cerebral vasospasm,
 CC pheochromocytoma, ganglioneuroblastoma, Huntington's disease, severe
 CC mental retardation, Alzheimer's disease, Parkinson's disease, psychotic
 CC depression, delirium, dementia and dyskinesias. The polypeptide may also
 CC be used in raising specific antibodies. The present nucleic acid sequence
 CC is that of the human NPY-like GPCR gene located on chromosome 11q12.2.
 CC This sequence encodes the human NPY-like GPCR protein of the invention.
 CC This sequence is also included in the human NPY-like GPCR DNA sequence
 CC (ABK14957) of the invention.
 XX

SQ Sequence 1296 BP; 344 A; 305 C; 301 G; 346 T; 0 other;

Query Match

Best Local Similarity 53.7%; Score 1296; DB 24; Length 1296;

Matches 1296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 354 ATGCGAGCGCTTAACATTACCGGAGCAGTTCTCTCGGCTGCTCGGAGCACCAACTG 413

Db 1 ATGCGAGCGCTTAACATTACCGGAGCAGTTCTCTCGGCTGCTCGGAGCACCAACTG 60

QY 414 ACGGGGAGCAGTTTCATCGCTCTGTACCGGCTGCGACCGCTCGTCTACACCCAGAGCTG 473

Db 61 ACGGGGAGCAGTTTCATCGCTCTGTACCGGCTGCGACCGCTCGTCTACACCCAGAGCTG 120

QY 474 CCGGAGCGCGCAAGCTGCGCTGCTCACCGGCTGCTCATCTTCGCGCTCGGCTC 533

Db 121 CCGGAGCGCGCAAGCTGCGCTGCTCACCGGCTGCTCATCTTCGCGCTCGGCTC 180

QY 534 TTGGCAATGCTCTGGGTGTTCTAGTGTGTCACCGGAGCGGCGCATGCCAGCTCACC 593

Db 181 TTGGCAATGCTCTGGGTGTTCTAGTGTGTCACCGGAGCGGCGCATGCCAGCTCACC 240

QY 594 AACATCTTTATCTGCTCTCTTTGGGCTCAGTGACCTGCTCATCTTCTTCGATTCCTC 653

Db 241 AACATCTTTATCTGCTCTCTTTGGGCTCAGTGACCTGCTCATCTTCTTCGATTCCTC 300

QY 654 GTACCATGCTCCAGAACATTCGCAAACTGGCTGGGGGTGCTTTCAATTTGCAAGATG 713

Db 301 GTACCATGCTCCAGAACATTCGCAAACTGGCTGGGGGTGCTTTCAATTTGCAAGATG 360

QY 714 GTGCCATTTGTCAGTCTACGGCTGTTGCACAGAAATCCTCATATGACCTGATTCCT 773

Db 361 GTGCCATTTGTCAGTCTACGGCTGTTGCACAGAAATCCTCATATGACCTGATTCCT 420

QY 774 GTGAAAAGGCACCGGACCTTGTGCATCTCTTTTAAATGAAGTGGCAATACACCAACCGA 833

Db 421 GTGAAAAGGCACCGGACCTTGTGCATCTCTTTTAAATGAAGTGGCAATACACCAACCGA 480

QY 834 AGGCTTTTCAATGCTAGTGTTGGTCTGGCTGGTGGCAGTCTATCTGATGATCACTCCT 893

Db 481 AGGCTTTTCAATGCTAGTGTTGGTCTGGCTGGTGGCAGTCTATCTGATGATCACTCCT 540

QY 894 TGGCAGCTGCAACAACTTGAGATCAAAATATGCTTCTATATGAAAAGGACACATCTGC 953

Db 541 TGGCAGCTGCAACAACTTGAGATCAAAATATGCTTCTATATGAAAAGGACACATCTGC 600

QY 954 TGCTTAGAAGATGGACCGACCTGTGTCACCAAGATCTACACCACTTCATCTCTGTC 1013

Db 601 TGCTTAGAAGATGGACCGACCTGTGTCACCAAGATCTACACCACTTCATCTCTGTC 660

QY 1014 ATCTCTTCTCTCTCTCTCTTATGGTGATGCTTATCTGTACAGTAAATTTGTTATGAA 1073

Db 661 ATCTCTTCTCTCTCTCTCTTATGGTGATGCTTATCTGTACAGTAAATTTGTTATGAA 720

QY 1074 CTTTGGATAAAGAAAAGAGTTGGGATGTTCTGATGCTTCAACTATTCTATGAAAAGAA 1133

Db 721 CTTTGGATAAAGAAAAGAGTTGGGATGTTCTGATGCTTCAACTATTCTATGAAAAGAA 780

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QY 1134 ATGTCAAAATAGCCAGGAGAGAAACGAGCTGTCAATTATGATGTTGACAGTGGTGGCT 1193
Db 781 ATGTCAAAATAGCCAGGAGAGAAACGAGCTGTCAATTATGATGTTGACAGTGGTGGCT 840
QY 1194 CTCCTTGTGTGTGCTGGGACCACTCCATGTTGTCATATGATGATGAATACAGTAAT 1253
Db 841 CTCCTTGTGTGTGCTGGGACCACTCCATGTTGTCATATGATGATGAATACAGTAAT 900
QY 1254 TTGTGAAGGAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1313
Db 901 TTGTGAAGGAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960
QY 1314 GGATTTTCCAACTCCATCTGTATCCCAATGTCATGCTATGATGATGATGATGATGATGAT 1373
Db 961 GGATTTTCCAACTCCATCTGTATCCCAATGTCATGCTATGATGATGATGATGATGATGAT 1020
QY 1374 AAAAATGTTTGTCTGAGTTGTTATGTCATGATGATGATGATGATGATGATGATGATGAT 1433
Db 1021 AAAAATGTTTGTCTGAGTTGTTATGTCATGATGATGATGATGATGATGATGATGATGAT 1080
QY 1434 AGGCATGGAATTCAGGAATTAACAATGATGCGGAGAGAAAGCAAGTTTCCCTCAGAGAG 1493
Db 1081 AGGCATGGAATTCAGGAATTAACAATGATGCGGAGAGAAAGCAAGTTTCCCTCAGAGAG 1140
QY 1494 AATCCAGTGGAGAAACCAAGAGAGAGCAATTCAGTGTGCGCAACATTCGAAGTCAAAATG 1553
Db 1141 AATCCAGTGGAGAAACCAAGAGAGAGCAATTCAGTGTGCGCAACATTCGAAGTCAAAATG 1200
QY 1554 TGTGACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1613
Db 1201 TGTGACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1260
QY 1614 CTGGCTGAGAAATCTCTTTAGACAGTGGGCATTAA 1649
Db 1261 CTGGCTGAGAAATCTCTTTAGACAGTGGGCATTAA 1296

RESULT 9
ID AAD01136
XX AAD01136 standard; cDNA; 1296 BP.
AC AAD01136;
XX AAD01136;
DT 02-NOV-2000 (first entry)
XX Human orphan G protein-coupled receptor hRUP4 cDNA.
DE Human; orphan G protein-coupled receptor; GPCR; hRUP4; drug screening;
KW transmembrane receptor; expressed sequence tag; EST; signal cascade; ss.
XX Homo sapiens.
OS
XX Key
FH Location/Qualifiers
CDS 1..1296
FT /tag= a
FT /product= "hRUP4"
FT /note= "Human orphan G protein-coupled receptor"
XX
PN WO200031258-A2.
XX
PD 02-JUN-2000.
XX
PF 13-OCT-1999; 99WO-US23687.
XX
XX 20-NOV-1998; 98US-0109213.
PR 16-FEB-1999; 98US-0120416.
PR 26-FEB-1999; 98US-0121852.
PR 12-MAR-1999; 99US-0123946.
PR 12-MAR-1999; 99US-0123949.
PR 28-MAY-1999; 99US-0136436.
PR 28-MAY-1999; 99US-0136437.
PR 28-MAY-1999; 99US-0136439.

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PR 28-MAY-1999; 99US-0136567.
PR 28-MAY-1999; 99US-0137127.
PR 28-MAY-1999; 99US-0137131.
PR 29-JUN-1999; 99US-0141448.
PR 29-SEP-1999; 99US-0156555.
PR 29-SEP-1999; 99US-0156633.
PR 29-SEP-1999; 99US-0156634.
PR 29-SEP-1999; 99US-0156653.
PR 01-OCT-1999; 99US-0157280.
PR 01-OCT-1999; 99US-0157281.
PR 01-OCT-1999; 99US-0157282.
PR 01-OCT-1999; 99US-0157293.
PR 01-OCT-1999; 99US-0157294.
PR 12-OCT-1999; 99US-0416760.
PR 12-OCT-1999; 99US-0417044.
XX (AREN-) ARENA PHARM INC.
XX Chen R, Dang HT, Liaw CW, Lin I;
PI P-PSDB; AAY71309.
XX WPI: 2000-400068/34.
XX PT Novel human orphan G protein-coupled receptors and the encoding cDNAs
PS for use in the identification of G protein-coupled receptor agonists -
XX Claim 73; Page 88-89; 102pp; English.
XX The present sequence is a cDNA encoding hRUP4, an endogenous human
CC orphan G protein-coupled receptor (GPCR). The full length hRUP4 cDNA was
CC cloned by RT-PCR with human brain cDNA as template. The hRUP4 PCR
CC fragment obtained was an alternatively spliced form of the EST (expressed
CC sequence tag) Clone AI307658. The orphan GPCR of the invention, like
CC all GPCRs has seven transmembrane alpha helices with an extracellular
CC N-terminus and an intracellular C-terminus. However, no endogenous
CC orphan GPCRs may be used in the identification of their endogenous
CC ligands, and to screen potential GPCR agonists and antagonists for use as
CC pharmaceutical agents. The proteins may also be used in the study of
CC GPCR-mediated signalling cascades, and to elucidate their precise role in
CC normal and diseased human conditions. Nucleic acid encoding human orphan
CC GPCRs may be used for tissue localisation expression analysis to provide
CC information about their function in healthy and pathological states.
XX
SQ Sequence 1296 BP; 344 A; 304 C; 302 G; 346 T; 0 other;
Query Match 53.6%; Score 1294.4; DB 21; Length 1296;
Best Local Similarity 99.9%; Pred. No. 6.5e-196;
Matches 1295; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 354 ATGACGGCGCTTAACATTACCCGAGCAGTCTCTCGGCTGCTGCGGAGACACAACTG 413
Db 1 ATGACGGCGCTTAACATTACCCGAGCAGTCTCTCGGCTGCTGCGGAGACACAACTG 60
QY 414 ACGCGGAGCAGTTCATCGCTCTGTACCGGCTGCGACCGCTCTACACCCAGAGCTG 473
Db 61 ACGCGGAGCAGTTCATCGCTCTGTACCGGCTGCGACCGCTCTACACCCAGAGCTG 120
QY 474 CCGGAGCGCCCAAGCTGGCCCTCGTGTCTACCGCGGTGCTCATCTTCGCCCTGGCGCTC 533
Db 121 CCGGAGCGCCCAAGCTGGCCCTCGTGTCTACCGCGGTGCTCATCTTCGCCCTGGCGCTC 180
QY 534 TTTGGCAATGCTGTTGTTCTAGTGTGACCGCGAGGCGCATCGGACCGTCACTACC 593
Db 181 TTTGGCAATGCTGTTGTTCTAGTGTGACCGCGAGGCGCATCGGACCGTCACTACC 240
QY 594 AACATCTTTATCTGCTCTTGGCGCTCAGTACCTGCTCATCATCTTCTTGCAATCCC 653
Db 241 AACATCTTTATCTGCTCTTGGCGCTCAGTACCTGCTCATCATCTTCTTGCAATCCC 300
QY 654 GTCACCATGCTCCAGAAACATTTCCGAACTGGCTGGGGGTGCTTTCAITTTGCAAGATG 713
Db 301 GTCACCATGCTCCAGAAACATTTCCGAACTGGCTGGGGGTGCTTTCAITTTGCAAGATG 360

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QY 714 GTGCCATTGTCAGTCTACCGTGTGTGTGACAGAAATCTCTACTGACCTGCATTGCT 773
D 361 GTGCCATTGTCAGTCTACCGTGTGTGTGACAGAAATGCTCACTATGACCTGCATTGCT 420
QY 774 GTGGAAGCACCAGGACTGTGTGCATCTCTTTAAATGAAGTGGCAATACACCAACCGA 833
D 421 GTGGAAGCACCAGGACTGTGTGCATCTCTTTAAATGAAGTGGCAATACACCAACCGA 480
QY 834 AGGGCTTTTACAAATGCTAGTGTGGTCTGGCTGGTGGCAGTCATCGTAGGATCAACCATG 893
D 481 AGGGCTTTTACAAATGCTAGTGTGGTCTGGCTGGTGGCAGTCATCGTAGGATCAACCATG 540
QY 894 TGGCAGTGGCAACAACTTGAGATCAAAATATGATCTTCTATATGAAAAGGAACACATCTGC 953
D 541 TGGCAGTGGCAACAACTTGAGATCAAAATATGATCTTCTATATGAAAAGGAACACATCTGC 600
QY 954 TGCCTAGAGAGTGGACCCAGCCCTGTGCACCAAGATCTACACCACTTCATCCCTTGC 1013
D 601 TGCCTAGAGAGTGGACCCAGCCCTGTGCACCAAGATCTACACCACTTCATCCCTTGC 660
QY 1014 ATCCTCTTCTCCTGCTCTTATGGTGATGCTTATTTCTGACAGTAAATTTGGTTATGAA 1073
D 661 ATCCTCTTCTCCTGCTCTTATGGTGATGCTTATTTCTGACAGTAAATTTGGTTATGAA 720
QY 1074 CTTTGGATAAAGAAAAGATGGGGATGGTTCAGTGCTTCGAACTATTTCATGAAAAGAA 1133
D 721 CTTTGGATAAAGAAAAGATGGGGATGGTTCAGTGCTTCGAACTATTTCATGAAAAGAA 780
QY 1134 ATGCTCAAAATACCGAGGAGAGAACGAGCTGTCATTTATGATGTCGACAGTGGCT 1193
D 781 ATGCTCAAAATACCGAGGAGAGAACGAGCTGTCATTTATGATGTCGACAGTGGCT 840
QY 1194 CTCTTTGCTGTGCTGGGACCATTCATGTTGTCTCATATGATGATGAATACAGTAAT 1253
D 841 CTCTTTGCTGTGCTGGGACCATTCATGTTGTCTCATATGATGATGAATACAGTAAT 900
QY 1254 TTTGAAAAGGAATATGATGATGTCAATCAAGATGATTTTGGTATCGTGCATAATTT 1313
D 901 TTTGAAAAGGAATATGATGATGTCAATCAAGATGATTTTGGTATCGTGCATAATTT 960
QY 1314 GGATTTTCCAACTCCATCTGTAATCCATGTCATGTCATTTATGAATGAATCTTCAA 1373
D 961 GGATTTTCCAACTCCATCTGTAATCCATGTCATGTCATTTATGAATGAATCTTCAA 1020
QY 1374 AAAAATGTTTGTGTCAGTTTGTATTGTCATAGTAAATAAAACCTTCTCTCCAGCACAA 1433
D 1021 AAAAATGTTTGTGTCAGTTTGTATTGTCATAGTAAATAAAACCTTCTCTCCAGCACAA 1080
QY 1434 AGCATGGAAATTCAGGAATTAACAATGATCGGAGAGAACCAAGTTTCCCTCAGAGAG 1493
D 1081 AGCATGGAAATTCAGGAATTAACAATGATCGGAGAGAACCAAGTTTCCCTCAGAGAG 1140
QY 1494 AATCCAGTGGAGAAACCAAGAGAGCAATTCAGTGTGCGAACATGGAATCAAAATG 1553
D 1141 AATCCAGTGGAGAAACCAAGAGAGCAATTCAGTGTGCGAACATGGAATCAAAATG 1200
QY 1554 TGTGAACAGACAGAGAGAGAAAAGCTCAAAACGACATCTGCTCTTTAGTCTGAA 1613
D 1201 TGTGAACAGACAGAGAGAGAAAAGCTCAAAACGACATCTGCTCTTTAGTCTGAA 1260
QY 1614 CTGGCTGAGAAATCTCTTTTAGACAGTGGCATTA 1649
D 1261 CTGGCTGAGAAATCTCTTTTAGACAGTGGCATTA 1296
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RESULT 10

AAA46037

ID AAA46037 standard; cDNA; 1296 BP.

XX

AC AAA46037;

XX

DT 22-AUG-2000 (first entry)

```
XX DE Human G protein coupled receptor hRUP4 encoding cDNA SEQ ID NO:39.
XX XX Human; G protein coupled receptor; GPCR; transmembrane receptor;
XX KW identification; agonist; screening; therapeutic; pharmaceutical;
XX KW mutant; ss.
XX OS Homo sapiens.
XX PN WO200022131-A2.
XX PD 20-APR-2000.
XX PF 13-OCT-1999; 99WO-US24065.
XX PR 13-OCT-1998; 98US-0170496.
XX PR 12-NOV-1998; 98US-0108029.
XX PR 20-NOV-1998; 98US-0109213.
XX PR 27-NOV-1998; 98US-0110060.
XX PR 16-FEB-1999; 99US-0120416.
XX PR 26-FEB-1999; 99US-0121852.
XX PR 12-MAR-1999; 99US-0123944.
XX PR 12-MAR-1999; 99US-0123945.
XX PR 12-MAR-1999; 99US-0123946.
XX PR 12-MAR-1999; 99US-0123948.
XX PR 12-MAR-1999; 99US-0123949.
XX PR 12-MAR-1999; 99US-0123951.
XX PR 28-MAY-1999; 99US-0136436.
XX PR 28-MAY-1999; 99US-0136437.
XX PR 28-MAY-1999; 99US-0136439.
XX PR 28-MAY-1999; 99US-0137127.
XX PR 28-MAY-1999; 99US-0137127.
XX PR 28-MAY-1999; 99US-0137127.
XX PR 30-JUN-1999; 99US-0137567.
XX PR 27-AUG-1999; 99US-0141448.
XX PR 03-SEP-1999; 99US-0152524.
XX PR 29-SEP-1999; 99US-0156633.
XX PR 29-SEP-1999; 99US-0156655.
XX PR 29-SEP-1999; 99US-0156634.
XX PA (AREN-) ARENA PHARM INC.
XX XX Behan DP, Lehmann-Bruisma K, Chalmers DT, Chen R, Dang HT;
XX PI Gore M, Liaw CW, Lin I, Lowitz K, White C;
XX WPI; 2000-317986/27.
XX DR P-PSDB; AAB02843.
XX XX Non-endogenous, human G protein-coupled receptors for screening
XX PT receptor, inverse or partial agonists useful as therapeutic agents -
XX PS Example 1; Page 118-119; 187pp; English.
XX CC The present invention describes transmembrane receptors, preferably
XX CC human G protein coupled receptors (GPCR), for which the endogenous
XX CC ligand is unknown (orphan GPCR receptors). More specifically the present
XX CC invention relates to non-endogenous, constitutively activated versions
XX CC of a human GPCR. These non-endogenous human GPCRs can be useful for
XX CC the direct identification of candidate compounds as receptors agonists,
XX CC inverse agonists or partial agonists for use as pharmaceutical agents,
XX CC AAA46017 to AAA46126 and AAB02825 to AAB02859 represent sequences used in
XX CC the exemplification of the present invention.
XX XX Sequence 1296 BP; 344 A; 304 C; 302 G; 346 T; 0 other;
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Query Match

53.6%; Score 1294.4; DB 21; Length 1296;

Best Local Similarity 99.9%; Pred. No. 6.5e-196;

Matches 1295; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 354 ATGCAGGCGCTTAACATTACCCCGGAGCAGTCTCTCGGCTGTCGGGACCAACCTG 413

D 1 ATGCAGGCGCTTAACATTACCCCGGAGCAGTCTCTCGGCTGTCGGGACCAACCTG 60

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QY 414 AGCGGGAGCATTTCATCGCTCTGTACCGGCTGCGACCGCTCGTCTACACCCAGAGCTG 473
Db 61 AGCGGGAGCATTTCATCGCTCTGTACCGGCTGCGACCGCTCGTCTACACCCAGAGCTG 120
QY 474 CGGGAACGGCCCAAGCTGGCCCTCGTGTCAACGGCGTGTCTCATCTTCGCCCTGGCGCTC 533
Db 121 CGGGAACGGCCCAAGCTGGCCCTCGTGTCAACGGCGTGTCTCATCTTCGCCCTGGCGCTC 180
QY 534 TTGGCAATGCTCTGCTGTCTACGTGTGACGTGACCGCCAGCGAGGCCATGGCAACCGTCAAC 593
Db 181 TTGGCAATGCTCTGCTGTCTACGTGTGACCGCCAGCGAGGCCATGGCAACCGTCAAC 240
QY 594 AACATCTTTATCTGCTCTGCGCTCACTGACCTGCTCATCACCTCTCTCTGCAATTCCTC 653
Db 241 AACATCTTTATCTGCTCTGCGCTCACTGACCTGCTCATCACCTCTCTCTGCAATTCCTC 300
QY 654 GTCACCATGCTCCAGAACATTTCCGACAACTGGCTGGGGGGTGTCTTCAATTTGCAAGATG 713
Db 301 GTCACCATGCTCCAGAACATTTCCGACAACTGGCTGGGGGGTGTCTTCAATTTGCAAGATG 360
QY 714 GTGCCATTTGTCCAGTCTACGCTCTGTGTGACAGAAATCCTCACTATGACCTGCAATTCCT 773
Db 361 GTGCCATTTGTCCAGTCTACGCTCTGTGTGACAGAAATGCTCACTATGACCTGCAATTCCT 420
QY 774 GTGGAAGGCAACGAGGACTTTGTGCATCTTTTAAATGAAATGAAAGGAAACACATCTGC 833
Db 421 GTGGAAGGCAACGAGGACTTTGTGCATCTTTTAAATGAAATGAAAGGAAACACATCTGC 480
QY 834 AGGCTTTTCAATGCTAGGCTGTGCTGCTGGCTGGGAGTCACTGATAGATCAACCCATG 893
Db 481 AGGCTTTTCAATGCTAGGCTGTGCTGCTGGGAGTCACTGATAGATCAACCCATG 540
QY 894 TGGCAGCTGCAACACTTGCAGATCAATATGACTTCTCTATATGAAAGGAAACACATCTGC 953
Db 541 TGGCAGCTGCAACACTTGCAGATCAATATGACTTCTCTATATGAAAGGAAACACATCTGC 600
QY 954 TGCTTAGAGAGTGACAGAGCCCTGTGCACGAGAGATCTACACCACTTCATCTTGTGTC 1013
Db 601 TGCTTAGAGAGTGACAGAGCCCTGTGCACGAGAGATCTACACCACTTCATCTTGTGTC 660
QY 1014 ATCTCTTCTCTCTGCTCTTATGCTGATGCTTATCTGTACAGTAAATTTGGTTATGAA 1073
Db 661 ATCTCTTCTCTCTGCTCTTATGCTGATGCTTATCTGTACAGTAAATTTGGTTATGAA 720
QY 1074 CTTTGGATAAAGAAAGTTGGGATGTTTCAGTGTCTTGGAACTTATTCATGGAAGAA 1133
Db 721 CTTTGGATAAAGAAAGTTGGGATGTTTCAGTGTCTTGGAACTTATTCATGGAAGAA 780
QY 1134 ATGTCCAAATAGCAGGAAGAAAGAGCTGTCTATATGATGGTGACAGTGGTGGCT 1193
Db 781 ATGTCCAAATAGCAGGAAGAAAGAGCTGTCTATATGATGGTGACAGTGGTGGCT 840
QY 1194 CTCTTTGCTGTGTGGGACCATTCCTCATGTTGTCATATGATGATGATGATGATGATGAT 1253
Db 841 CTCTTTGCTGTGTGGGACCATTCCTCATGTTGTCATATGATGATGATGATGATGATGAT 900
QY 1254 TTTGAAAGGAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1313
Db 901 TTTGAAAGGAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960
QY 1314 GGATTTTCCAACTCATCTGTAATCCCATTTGTCATGATGATGATGATGATGATGATGATGAT 1373
Db 961 GGATTTTCCAACTCATCTGTAATCCCATTTGTCATGATGATGATGATGATGATGATGATGAT 1020
QY 1374 AAAAATGTTTGTCTGCACTTTGTTATTTGATGATGATGATGATGATGATGATGATGATGAT 1433
Db 1021 AAAAATGTTTGTCTGCACTTTGTTATTTGATGATGATGATGATGATGATGATGATGATGAT 1080
QY 1434 AGGCATGGAATTCAGGAATTTACATGATGATGATGATGATGATGATGATGATGATGATGATG 1493
Db 1081 AGGCATGGAATTCAGGAATTTACATGATGATGATGATGATGATGATGATGATGATGATGATG 1140
QY 1494 AATCCAGTGGGAAACCAAGGAGAGCATTTCAGTGTGCAACATGGAAGTCAAAATTG 1553
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Db 1141 AATCCAGTGGGAAACCAAGGAGAGCATTTCAGTGTGCAACATGGAAGTCAAAATTG 1200
QY 1554 TGTGAACAGACAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1613
Db 1201 TGTGAACAGACAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1260
QY 1614 CTGCTCAGAGATTTCTCTTTAGACAGTGGGCAATTAA 1649
Db 1261 CTGCTCAGAGATTTCTCTTTAGACAGTGGGCAATTAA 1296

RESULT 11
AAF81818
ID AAF81818 standard; cDNA; 1293 BP.
XX
AC AAF81818;
XX
DT 05-JUN-2001 (first entry)
XX
DE Human G protein-coupled receptor protein A027 encoding cDNA SEQ ID NO:2.
XX
KW Human; G protein-coupled receptor; A027; nootropic; neuroprotective;
hypotensive; antirheumatic; antiallergic; cardiant; antianigmal;
XX
KW abortifacient; gene therapy; Alzheimer's disease; hypertension;
pregnancy termination; rheumatism; allergy; angina pectoris; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
CDS 1..1293
FT /*tag= a
FT /partial
FT /product= "A027"
FT /note= "G protein coupled receptor; no stop codon given"
XX
PN W0200116316-A1.
XX
PD 08-MAR-2001.
XX
PF 24-AUG-2000; 2000WO-JP05684.
XX
PR 27-AUG-1999; 99JP-0241530.
XX
(PAKE ) TAKEDA CHEM IND LTD.
XX
Watanabe T, Kikuchi K, Shintani Y;
XX
WPI; 2001-226689/23.
XX
P-PSDB; AAB74773.
XX
Human brain-originated guanosine triphosphate protein-coupled receptor,
its salt and encoded gene, useful in (gene) diagnosis and development
of preventives and remedies for e.g. Alzheimer disease, hypertension
and rheumatism
XX
Claim 4; Page 78-79; 84pp; Japanese.
XX
The present sequence encodes a human G protein-coupled receptor
designated A027. A027 has nootropic, neuroprotective, hypotensive,
antirheumatic, antiallergic, cardiant, antianigmal and abortifacient
activities. A027 can be used as a G protein-coupled receptor protein
agonist, G-protein-coupled receptor signal transducer and in gene
therapy. A027 can be used in the diagnosis and development of
preventives and remedies for diseases associated with dysfunction of
A027 e.g. Alzheimer's disease, hypertension, pregnancy termination,
rheumatism, allergy and angina pectoris.
XX
SQ Sequence 1293 BP; 342 A; 305 C; 301 G; 345 T; 0 other;
Query Match 53.5%; Score 1293; DB 22; Length 1293;
Best Local Similarity 100.0%; Pred. No. 1.1e-195;
Matches 1293; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 354 ATGCAGCGGCTTAACATTACCCGAGAGAGTTCTCTCGGCTGCTGCGGACCAACACCTG 413
Db 1 ATGCAGCGGCTTAACATTACCCGAGAGAGTTCTCTCGGCTGCTGCGGACCAACACCTG 60
Qy 414 ACGGGAGAGAGTTATGCTGCTCTGTACCGGCTGGGACCGCTGCTGTACACCCAGAGTG 473
Db 61 ACGGGAGAGAGTTATGCTGCTCTGTACCGGCTGGGACCGCTGCTGTACACCCAGAGTG 120
Qy 474 CCGGAGCGCGCAAGCTGCGCTCTGTGCTACCGGCGTGTCTATCTTCGCCCTCGCGCTC 533
Db 121 CCGGAGCGCGCAAGCTGCGCTCTGTGCTACCGGCGTGTCTATCTTCGCCCTCGCGCTC 180
Qy 534 TTTGGCAATGCTCTGGTGTCTACGCTGTGACCGGCGTGTCTATCTTCGCCCTCGCGCTC 593
Db 181 TTTGGCAATGCTCTGGTGTCTACGCTGTGACCGGCGTGTCTATCTTCGCCCTCGCGCTC 240
Qy 594 AACATCTTTATCTGCTCTGCGGCTGAGTACCTGCTCATCAGCTTCTTGTGATTCCTC 653
Db 241 AACATCTTTATCTGCTCTGCGGCTGAGTACCTGCTCATCAGCTTCTTGTGATTCCTC 300
Qy 654 GTACCATGCTCCAGACATTCGACAACTGGCTGGGGGTGCTTTCATTTGCAAGATG 713
Db 301 GTACCATGCTCCAGACATTCGACAACTGGCTGGGGGTGCTTTCATTTGCAAGATG 360
Qy 714 GTGCCATTTGTCAGTCTACCGCTGTTGTGACAGAAATCTCTACTATGACCTGCAATGCT 773
Db 361 GTGCCATTTGTCAGTCTACCGCTGTTGTGACAGAAATCTCTACTATGACCTGCAATGCT 420
Qy 774 GTGAAAGGACACGAGGAGCTGTGATCTCTTTTAAATGAAAGTGGCAATACCAACCGA 833
Db 421 GTGAAAGGACACGAGGAGCTGTGATCTCTTTTAAATGAAAGTGGCAATACCAACCGA 480
Qy 834 AGGCTTTTCAATGCTAGTGTGCTGCTGGTGGCGAGTCATCGTAGGATCACCAGT 893
Db 481 AGGCTTTTCAATGCTAGTGTGCTGCTGGTGGCGAGTCATCGTAGGATCACCAGT 540
Qy 894 TGGCACGTGCAACAACTTGAGATCAATATATGACTTCTTATATGAAAGGAACACATCTGC 953
Db 541 TGGCACGTGCAACAACTTGAGATCAATATATGACTTCTTATATGAAAGGAACACATCTGC 600
Qy 954 TGCTTAGAGAGTGGACCGCCCTGTGACACAGAGATCTACACACCTTCACTCTGTGTC 1013
Db 601 TGCTTAGAGAGTGGACCGCCCTGTGACACAGAGATCTACACACCTTCACTCTGTGTC 660
Qy 1014 ATCTCTTCTCTCTGCTCTTATGCTGATGCTTATCTGTACAGTAAATGTTATGAA 1073
Db 661 ATCTCTTCTCTCTGCTCTTATGCTGATGCTTATCTGTACAGTAAATGTTATGAA 720
Qy 1074 CTTTGGATAAGAAAGAGTTGGGATGGTTCACTGCTTGGAACTATTCATGAAAGAA 1133
Db 721 CTTTGGATAAGAAAGAGTTGGGATGGTTCACTGCTTGGAACTATTCATGAAAGAA 780
Qy 1134 ATGTCCAAATAGCAGGAGAGAGAGAGCTGCTATATGATGAGTGGACAGTGGTCT 1193
Db 781 ATGTCCAAATAGCAGGAGAGAGAGAGCTGCTATATGATGAGTGGACAGTGGTCT 840
Qy 1194 CTCTTTGCTGTGCTGGGACCACTTCCATGTTGTCATATGATGATGATGATGATGAT 1253
Db 841 CTCTTTGCTGTGCTGGGACCACTTCCATGTTGTCATATGATGATGATGATGATGAT 900
Qy 1254 TTTGAAAGGAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1313
Db 901 TTTGAAAGGAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960
Qy 1314 GGATTTTCCACTCCATCTGTAATCCCATGCTATGCAATTTGATGATGATGATGATGAT 1373
Db 961 GGATTTTCCACTCCATCTGTAATCCCATGCTATGCAATTTGATGATGATGATGATGAT 1020
Qy 1374 AAAATGTTTTGCTGCAAGTTTGTATGATGATGATGATGATGATGATGATGATGATGAT 1433
Db 1021 AAAATGTTTTGCTGCAAGTTTGTATGATGATGATGATGATGATGATGATGATGATGAT 1080

Qy 1434 AGGCATGGAATTCAGGAATTACAATGATCGGAAGAAAGCAAAAGTTTCCCTCAGAGAG 1493
Db 1081 AGGCATGGAATTCAGGAATTACAATGATCGGAAGAAAGCAAAAGTTTCCCTCAGAGAG 1140
Qy 1494 AATCCAGTGAGGAACCAAGGAGAGCAATTCAGTGTATGGCAACATGGAAGTCAAAATG 1553
Db 1141 AATCCAGTGAGGAACCAAGGAGAGCAATTCAGTGTATGGCAACATGGAAGTCAAAATG 1200
Qy 1554 TGTGAACAGACAGAGAGAGAGAAAGAGCTCAACAGACATCTTGTCTCTTTAGGCTGAA 1613
Db 1201 TGTGAACAGACAGAGAGAGAGAAAGAGCTCAACAGACATCTTGTCTCTTTAGGCTGAA 1260
Qy 1614 CTGGCTGAGAATTCCTCTTTAGACAGTGGGCAT 1646
Db 1261 CTGGCTGAGAATTCCTCTTTAGACAGTGGGCAT 1293
RESULT 12
AAA46115
ID AAA46115 standard; cDNA; 1296 BP.
XX AC AAA46115;
XX AC
XX AC
DT 22-AUG-2000 (first entry)
XX
DE Human G protein coupled receptor hRUP4 (V272K) cDNA SEQ ID NO:127.
XX
KW Human; G protein coupled receptor; GPCR; transmembrane receptor;
KW identification; agonist; screening; therapeutic; pharmaceutical;
KW mutant; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
XX
DN W0200022131-A2.
XX
PD 20-APR-2000.
XX
PP 13-OCT-1999; 99WO-US24065.
XX
PR 13-OCT-1998; 98US-0170496.
PR 12-NOV-1998; 98US-0108029.
PR 20-NOV-1998; 98US-0109213.
PR 27-NOV-1998; 98US-0110060.
PR 16-FEB-1999; 99US-0120416.
PR 26-FEB-1999; 99US-0121852.
PR 12-MAR-1999; 99US-0123944.
PR 12-MAR-1999; 99US-0123945.
PR 12-MAR-1999; 99US-0123946.
PR 12-MAR-1999; 99US-0123948.
PR 12-MAR-1999; 99US-0123949.
PR 12-MAR-1999; 99US-0123951.
PR 28-MAY-1999; 99US-0136436.
PR 28-MAY-1999; 99US-0136437.
PR 28-MAY-1999; 99US-0136439.
PR 28-MAY-1999; 99US-0137127.
PR 28-MAY-1999; 99US-0137131.
PR 30-JUN-1999; 99US-0137567.
PR 27-AUG-1999; 99US-0151114.
PR 03-SEP-1999; 99US-0152524.
PR 29-SEP-1999; 99US-0156633.
PR 29-SEP-1999; 99US-0156555.
PR 29-SEP-1999; 99US-0156634.
XX
PA (AREN-) ARENA PHARM INC.
XX
XX Behan DP, Lehmann-Bruinsma K, Chalmers DT, Chen R, Dang HT;
PI Gore M, Liaw CW, Lin I, Lowitz K, White C;
XX WPI; 2000-317986/27.
DR P-PSDB; AAB02853.
XX

PT Non-endogenous, human G protein-coupled receptors for screening
 PT receptor, inverse or partial agonists useful as therapeutic agents
 XX
 PS Example 2; Page 163-164; 187pp; English.

CC The present invention describes transmembrane receptors, preferably
 CC human G protein coupled receptors (GPCR), for which the endogenous
 CC ligand is unknown (orphan GPCR receptors). More specifically the present
 CC invention relates to non-endogenous, constitutively activated versions
 CC of a human GPCR. These non-endogenous human GPCRs can be useful for
 CC the direct identification of candidate compounds as receptors agonists,
 CC inverse agonists or partial agonists for use as pharmaceutical agents.
 CC AAA46017 to AAA46126 and AAB02825 to AAB02859 represent sequences used in
 CC the exemplification of the present invention.

XX Sequence 1296 BP; 346 A; 303 C; 302 G; 345 T; 0 other;

Query Match 53.4%; Score 1289.6; DB 21; Length 1296;
 Best Local Similarity 99.7%; Pred. No. 3.7e-195;
 Matches 1292; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 354 ATGCAGGGCGCTTAACATTACCCCGGAGCAGTCTCTCGGCTGCTCGGGACCAACCTG 413
 Db 1 ATGCAGGGCGCTTAACATTACCCCGGAGCAGTCTCTCGGCTGCTCGGGACCAACCTG 60
 QY 414 ACGGGGAGCAGTTTCATCGCTCTGTACCGGCTGCGACCGCTCGTCTACACCCGAGCTG 473
 Db 61 ACGGGGAGCAGTTTCATCGCTCTGTACCGGCTGCGACCGCTCGTCTACACCCGAGCTG 120
 QY 474 CCGGACCGCGCAAGCTGGCCCTCTGTCTACCGCGCTGCTCATTTTGGCCCTGGCGTCC 533
 Db 121 CCGGACCGCGCAAGCTGGCCCTCTGTCTACCGCGCTGCTCATTTTGGCCCTGGCGTCC 180
 QY 534 TTTGGCAATGCTCTGCTGTTTCTACCTGTGTGACCGCAGCAGGCGCATCGCAGCTCACC 593
 Db 181 TTTGGCAATGCTCTGCTGTTTCTACCTGTGTGACCGCAGCAGGCGCATCGCAGCTCACC 240
 QY 594 AACATCTTTATCTGCTCTTGGCGCTCAGTCACTGCTCATCACCTTCTTCTGCAATCCC 653
 Db 241 AACATCTTTATCTGCTCTTGGCGCTCAGTCACTGCTCATCACCTTCTTCTGCAATCCC 300
 QY 654 GTCACCATGCTCCAGAACATTCGACAACTGGCTGGGGGGTGTCTTCAATTTGCAAGATG 713
 Db 301 GTCACCATGCTCCAGAACATTCGACAACTGGCTGGGGGGTGTCTTCAATTTGCAAGATG 360
 QY 714 GTGCCAATTTGTCAGTCTACCGCTGTTGTGACAGAAATCCCTCACTATGACCTGCAATGCT 773
 Db 361 GTGCCAATTTGTCAGTCTACCGCTGTTGTGACAGAAATGCTCACTATGACCTGCAATGCT 420
 QY 774 GTGAAAGGCGCCAGGGACTTGTGCATCCTTTTAAATGAAAGTGGCAATACCAACCGA 833
 Db 421 GTGAAAGGCGCCAGGGACTTGTGCATCCTTTTAAATGAAAGTGGCAATACCAACCGA 480
 QY 834 AGGCTTTTCAATGCTAGGTGTGTCTGGCTGGTGGGAGTCATGCTAGGATCACCATG 893
 Db 481 AGGCTTTTCAATGCTAGGTGTGTCTGGCTGGTGGGAGTCATGCTAGGATCACCATG 540
 QY 894 TGGCAGCTGCACAACTTGAGATCAAAATATGACTTCTTATATGAAAGGAAACATCTGC 953
 Db 541 TGGCAGCTGCACAACTTGAGATCAAAATATGACTTCTTATGAAAGGAAACATCTGC 600
 QY 954 TGCTTAGAAGGTGAGCCAGCCCTGTGACCAAGAGATCTACACCACCTTCATCCTTGTG 1013
 Db 601 TGCTTAGAAGGTGAGCCAGCCCTGTGACCAAGAGATCTACACCACCTTCATCCTTGTG 660
 QY 1014 ATCCTCTTCTCTGCTCTTATGCTGATGCTTATCTGTACAGTAAATTTGTTATGAA 1073
 Db 661 ATCCTCTTCTCTGCTCTTATGCTGATGCTTATCTGTACAGTAAATTTGTTATGAA 720
 QY 1074 CTTTGGATAAAGAAAGAGTTGGGGATGTTTCACTGCTTCGAACTATTTCATGGAAAGAA 1133
 Db 721 CTTTGGATAAAGAAAGAGTTGGGGATGTTTCACTGCTTCGAACTATTTCATGGAAAGAA 780

QY 1134 ATGTCCAAATAGCCAGGACGAAAGACGAGCTGTCATTATGATGGTGACAGTGGTGCT 1193
 Db 781 ATGTCCAAATAGCCAGGACGAAAGACGAGCTGTCATTATGATGGTGACAGTGGTGCT 840
 QY 1194 CTCCTTGTGTGTCTGGGACCACTTCATGTTCTCCATATGATGATTGAATACAGTAAT 1253
 Db 841 CTCCTTGTGTGTCTGGGACCACTTCATGTTCTCCATATGATGATTGAATACAGTAAT 900
 QY 1254 TTTGAAAGGAATATGATGATGTCAATCAAGATGATTTTGTCTATCGTGCAATATT 1313
 Db 901 TTTGAAAGGAATATGATGATGTCAATCAAGATGATTTTGTCTATCGTGCAATATT 960
 QY 1314 GGATTTTCCACTCCATCTGTCTGATCCCATGCTATGATGATGATGATGATGATGAT 1373
 Db 961 GGATTTTCCACTCCATCTGTCTGATCCCATGCTATGATGATGATGATGATGATGATGAT 1020
 QY 1374 AAAAATGTTTGTCTGAGTTTGTATTGATAGTAAATAAAACCTTCTCTCCAGCAAA 1433
 Db 1021 AAAAATGTTTGTCTGAGTTTGTATTGATAGTAAATAAAACCTTCTCTCCAGCAAA 1080
 QY 1434 AGGCATGGAATTCAGGAATTAATGATGCGGAGAAAGCAAGTTTTCCTCAGAGAG 1493
 Db 1081 AGGCATGGAATTCAGGAATTAATGATGCGGAGAAAGCAAGTTTTCCTCAGAGAG 1140
 QY 1494 AATCCAGTGGAGAAACCAAGGAGAGCATTCAATGATGCGGAGAAAGCAAGTTTTCCTCAGAGAG 1553
 Db 1141 AATCCAGTGGAGAAACCAAGGAGAGCATTCAATGATGCGGAGAAAGCAAGTTTTCCTCAGAGAG 1200
 QY 1554 TGTGAAACAGACAGAGGAGAAAGCAAGTTTTCCTCAGAGAGCATTCTCTCTTTAGTCTGAA 1613
 Db 1201 TGTGAAACAGACAGAGGAGAAAGCAAGTTTTCCTCAGAGAGCATTCTCTCTTTAGTCTGAA 1260
 QY 1614 CTGGCTCAGAAATCTCTCTTTAGACAGTGGGCAATTA 1649
 Db 1261 CTGGCTCAGAAATCTCTCTTTAGACAGTGGGCAATTA 1296

RESULT 13
 ABZ42861
 ID ABZ42861 standard; DNA; 1368 BP.
 XX AC ABZ42861;
 XX AC
 DT 04-MAR-2003 (first entry)
 XX
 DE Human G protein-coupled receptor GPR103 nucleotide SEQ ID NO:509.
 XX
 KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
 KW G protein-coupled receptor modulator; antibody; immune-related disease;
 KW growth-related disease; cell regeneration-related disease; AIDS; cancer;
 KW immunological-related cell proliferative disease; autoimmune disease;
 KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
 KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
 KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
 KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
 KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
 KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
 KW ulcer; gene; ds.
 XX
 OS Homo sapiens.
 XX
 XX W0200261087-A2.
 XX
 XX 08-AUG-2002.
 XX
 XX 19-DEC-2001; 2001WO-US50107.
 XX
 XX 19-DEC-2000; 2000US-257144P.
 XX
 XX (LIFE-) LIFESPAN BIOSCIENCES INC.
 XX
 XX Burmer GC, Roush CL, Brown JP;
 XX

DR WPI; 2003-046718/04.
 DR P-PSDB; ABP82011.

PT New isolated antigenic peptides e.g., for G protein-coupled receptors
 PT (GPCR), useful for diagnosing and designing drugs for treating
 PT conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease,
 PT cancer or autoimmune diseases

XX Disclosure; Fig 1; 523pp; English.

XX The present invention describes antigenic peptides (I) comprising:
 CC (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
 CC acids, also described: (1) an assay for the detection of a particular
 CC G protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
 CC and (2) an isolated antibody having high specificity and high affinity
 CC or avidity for a particular GPCR. (I) can be used as GPCR modulators and
 CC in gene therapy. The antigenic peptides for GPCRs are useful in detecting
 CC an antibody against a particular GPCR, and in the production of specific
 CC antibodies. The peptides and antibodies are also useful for detecting the
 CC presence or absence of corresponding GPCRs. The antigenic peptides for
 CC GPCRs and antibodies are useful for diagnosing and designing drugs for
 CC treating immune-related diseases, growth-related diseases, cell
 CC regeneration-related disease, immunological-related diseases, cell
 CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
 CC atherosclerosis, bacterial, fungal, protozoan or viral infections,
 CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
 CC inflammation, allergies, Crohn's disease, diabetes, graft versus host
 CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
 CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
 CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
 CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
 CC any other disorder in which GPCRs are involved. The antibodies may be
 CC used in immunoassays and immunodiagnosis. AB242523 to AB242869 encode
 CC GPCR proteins given in ABP81675 to ABP82018, which are used in the
 CC exemplification of the present invention.

XX Sequence 1368 BP; 345 A; 346 C; 319 G; 358 T; 0 other;

Query Match 44.7%; Score 1078.4; DB 25; Length 1368;
 Best Local Similarity 91.3%; Pred. No. 8.9e-162;
 Matches 1213; Conservative 0; Mismatches 1; Indels 114; Gaps 2;

QY 322 GCGGTGGCCCGCGTCCCGGAGCGGACACAGCATGAGCGGCTTAACATTACCCGGAGC 381
 DB 155 GCGGTGGCCCGCGTCCCGGAGCGGACACAGCATGAGCGGCTTAACATTACCCGGAGC 214
 QY 382 AGTTCTCTCGGTGCTGCGGGACCAACCTGACGGCGGAGCAGTTCATCGTCTGTACC 441
 DB 215 AGTTCTCTCGGTGCTGCGGGACCAACCTGACGGCGGAGCAGTTCATCGTCTGTACC 274
 QY 442 GCGTGGACCGGTGCTGCTACACCCAGAGTGGCGGACGCGCAAGTGGCCCTCGTGC 501
 DB 275 GCGTGGACCGGTGCTGCTACACCCAGAGTGGCGGACGCGCAAGTGGCCCTCGTGC 334
 QY 502 TCACCGGCGGTGCTCATCTTCGCGCTGGCGCTCTTTGGCAATGCTCTGGTCTACGGTG 561
 DB 335 TCACCGGCGGTGCTCATCTTCGCGCTGGCGCTCTTTGGCAATGCTCTGGTCTACGGTG 394
 QY 562 TCACCGGACGAGGCGCATGCGCACCGTCCACCAACATCTTTATCTGCTCCTTGGGCTCA 621
 DB 395 TCACCGGACGAGGCGCATGCGCACCGTCCACCAACATCTTTATCTGCTCCTTGGGCTCA 454
 QY 622 GTGACCTGCTCATCACCCTCTCTTGATTCGGGTACCATGCTCCAGAACATTTCCGACA 681
 DB 455 GTGACCTGCTCATCACCCTCTCTTGATTCGGGTACCATGCTCCAGAACATTTCCGACA 514
 QY 682 ACTGGCTGGGGGTGCTTTTCATTTGCAAGATGGTGCCATTTGTCAGTACCGCTGTG 741
 DB 515 ACTGGCTGGGGGTGCTTTTCATTTGCAAGATGGTGCCATTTGTCAGTACCGCTGTG 574
 QY 742 TGACAGAAATCTCTCACTATGACCTGCTGCTGTGAAAGGACCCAGGACTTGTGCATC 801
 DB 575 TGACAGAAATCTCTCACTATGACCTGCTGCTGTGAAAGGACCCAGGACTTGTGCATC 634

QY 802 CTTTAAATGAAGTGGCAATACCAACCGAAGGGCTTTCTCAATGCTAGGTGTGGTCT 861
 DB 635 CTTTAAATGAAGTGGCAATACCAACCGAAGGGCTTTCTCAATGCTAGGTGTGGTCT 694
 QY 862 GCGTGGTGGCAGTCATCGTAGGATCACCCATGTGGCAGCTGCAACAACTTGAGATCAAT 921
 DB 695 GCGTGGTGGCAGTCATCGTAGGATCACCCATGTGGCAGCTGCAACAACTTGAGATCAAT 754
 QY 922 ATGACTTCTTATATGAAAGGAACACATCTGCTGCTTAGAAGTGGACAGCCCTGTGC 981
 DB 755 ATGACTTCTTATATGAAAGGAACACATCTGCTGCTTAGAAGTGGACAGCCCTGTGC 814
 QY 982 ACCAGAGATCTACACCACTTCACTCTTGTCTCATCTCTCTCTCTCTCTCTCTCTCTCT 1041
 DB 815 ACAGAGAGATCTACACCACTTCACTCTTGTCTCTCTCTCTCTCTCTCTCTCTCTCT 868
 QY 1042 TCGTTATCTGTACAGTAAATTTGGTATGAACTTTGGATAAGAAAGAGTTGGGATG 1101
 DB 869 ----- 868
 QY 1102 GTTCAGTGTTCGAACTATTCTGGAAGAAATGTCCAAATAGCCAGAAAGAAAC 1161
 DB 869 -----GGAAGAAAGAAAC 880
 QY 1162 GAGCTGTCAATTATGATGGTGAGTGGTCTCTTTCTGCTGCTGCTGGCACCATTCTC 1221
 DB 881 GAGCTGTCAATTATGATGGTGAGTGGTGGCTCTCTTTCTGCTGCTGGCACCATTCTC 940
 QY 1222 AGTTGTCTCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1281
 DB 941 ATGTTGTCCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1000
 QY 1282 TCAAGATGATTTTGTCTATCGTGCAATTTATGGAATTTTCCAACTCCATCTGTAATCCCA 1341
 DB 1001 TCAAGATGATTTTGTCTATCGTGCAATTTATGGAATTTTCCAACTCCATCTGTAATCCCA 1060
 QY 1342 TTGCTCTATGCAATTATGATGAAACTTTCAAAAAAATGTTTTGCTGCTGAGTTGTATT 1401
 DB 1061 TTGCTCTATGCAATTATGATGAAACTTTCAAAAAAATGTTTTGCTGCAAGTTGTATT 1120
 QY 1402 GATAGTAAATAAAACCTTTCTCTCCAGCACAAAGGATGGAATTCAGGAATTAACAATCA 1461
 DB 1121 GCATAGTAAATAAAACCTTTCTCTCCAGCACAAAGGATGGAATTCAGGAATTAACAATCA 1180
 QY 1462 TCGCGAAGAAAGCAAGTCTTCCCTCAGAGAGATTCAGTGGAGAAACCAAGAGAGAG 1521
 DB 1181 TCGCGAAGAAAGCAAGTCTTCCCTCAGAGAGATTCAGTGGAGAAACCAAGAGAGAG 1240
 QY 1522 CATTCAGTGTGCGCAACATTCGAATTCATGTAAGTCAAAATGTTGTAACAGACAGAGAGAGAGAGAG 1581
 DB 1241 CATTCAGTGTGCGCAACATTCGAATTCATGTAAGTCAAAATGTTGTAACAGACAGAGAGAGAGAGAG 1300
 QY 1582 TCACACGACATCTGCTCTCTTTAGTCTGAATCTGGCTGAGAATTTCTCTTTAGACAGTG 1641
 DB 1301 TCAACACGACATCTGCTCTCTTTAGTCTGAATCTGGCTGAGAATTTCTCTTTAGACAGTG 1360
 QY 1642 GGCATTAA 1649
 DB 1361 GGCATTAA 1368

RESULT 14

ABK86292

ID ABK86292 standard; cDNA; 1737 BP.

XX ABK86292;

AC ABK86292;

XX 27-AUG-2002 (first entry)

XX Mouse TGR346a cDNA.

XX Mouse; TGR346a; gene; ss; G-protein coupled receptor; GPCR; TGR;

TGR-associated disorder; signal transduction; renal failure; nephritis; hypothyroidism; hypogonadism; retinitis pigmentosa; growth disorder; diabetes insipidus; hyperprolactinaemia; thirst disturbance; appetite; sleep disturbance; temperature regulation; blood pressure; hypothalamus; circadian rhythm.

OS Mus sp.

Key Location/Qualifiers
CDS 1..1302
FT /*tag= a
FT /product= "Mouse TGR346a protein"

XX W0200242458-A2.

XX 30-MAY-2002.

XX 21-NOV-2001; 2001WO-US43404.

XX 22-NOV-2000; 2000US-252841P.

XX 22-DEC-2000; 2000US-257636P.

XX 12-JAN-2001; 2001US-261377P.

XX 28-MAR-2001; 2001US-279554P.

XX 29-MAR-2001; 2001US-280696P.

XX (TULA-) TULARIK INC.

XX Tian H, Zhao J, Chen J, Cutler G, An S, Dai K, Gupte JS;

XX WPI; 2002-463633/49.

XX P-PSDB; AAU97740.

XX New isolated G-protein coupled receptor polypeptide, termed TGR, for diagnosis and treatment of diseases such as renal failure, nephritis, hypothyroidism, diabetes insipidus, and disturbances of thirst and sleep.

XX Claim 22; Page 77-78; 98pp; English.

XX The invention relates to a G-protein coupled receptor polypeptide (GPCR), termed TGR, and its associated nucleic acid. The sequences of the invention are useful for identifying a compound that modulates signal transduction and for identifying a mammal having a TGR-associated disorder. The proteins and nucleic acids are useful in diagnosis and treatment of diseases or conditions such as renal failure, nephritis, hypothyroidism, hypogonadism, retinitis pigmentosa, growth disorders, diabetes insipidus, hyperprolactinaemia and disturbances of thirst, sleep, temperature regulation, appetite, blood pressure or any other syndrome or disease associated with the hypothalamus. The sequences can be used in regulation of circadian rhythms, for use as genetic markers for the identification of mutations associated with diseases resulting from GPCR inactivation in particular cell types and for identification of modulators of GPCR signal transduction. This sequence represents cDNA encoding the mouse TGR346a polypeptide.

XX Sequence 1737 BP; 473 A; 384 C; 392 G; 488 T; 0 other;

Query Match 41.2%; Score 994.6; DB 24; Length 1737;
Best Local Similarity 81.2%; Pred. No. 1.6e-148;
Matches 1172; Conservative 0; Mismatches 259; Indels 12; Gaps 1;

QY 354 ATCCAGCGCTTACATTACCCGAGCAGTTCTCTCGGCTGCTGGGACCAACACCTG 413
DB 1 ATCCAGCGCTTACATTACCCGAGCAGTTCTCTCGGCTGCTGGGACCAACACCTG 60

QY 414 ACGGGGAGCAGTTTCATCGCTCTGTACCGCTGCGACCGCTGCTACACCCCGAGAGCTG 473
DB 61 ACTCGGAACAGTTTCATTCATCGCTGCGACCGCTGCTACATCCCGAGCTG 120

QY 474 CCGGAGCGCCCAAGCTGGCCCTGTGCTCACCGGGTGTCTATCTTCGCCCTGGGGCTC 533
DB 121 CCGGCGCGCTAACTGGGCTTTGGCTGGCTGGAGCACTCATTTTGGCCCTGGCGCTC 190

QY 534 TTGGCAATGCTCTGGTGTTCTACGTGGTGACCGCAGCAAGCCATGCGCACCGTCCACC 593
DB 181 TTGGCAATGCTCTGGTGTTCTACGTGGTGACCGCAGCAAGCCATGCGCACCGTCCACC 240
QY 594 AACATCTTTATCTGCTCTTTGGGCTCAGTGCAGCTGCTCATCACCTTCTTCTGCAATCCC 653
DB 241 AACATCTTTATCTGCTCTTTGGGCTCAGTGCAGCTGCTCATCACCTTCTTCTGCAATCCC 300
QY 654 GTCACCATGCTCCAGAACATTTCCGCAACTGCTGGGGGTGCTTTCATTTGCAAGATG 713
DB 301 GTCACCATGCTCCAGAACATTTCCGCAACTGCTGGGGGTGCTTTCATTTGCAAGATG 360
QY 714 GTCCCATTTTGTCCAGTCTACCGCTGTTGTGACAGAAATCTCATCTGCTTCTGCAATGCT 773
DB 361 GTCCCATTTTGTCCAGTCTACCGCTGTTGTGACAGAAATCTCATCTGCTTCTGCAATGCT 420
QY 774 GTGGAAGGCAACAGGCACTTTGTCATTCCTTTTAAATGAAGTGGCAATACACCAACCGA 833
DB 421 GTTGAGAGGCAACAGGCACTTTGTCATTCCTTTTAAATGAAGTGGCAATACACCAACCGA 480
QY 834 AGGCTTTTACCAATGCTAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 893
DB 481 AGGCTTTTACCAATGCTAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
QY 894 TGGCAGTGCACAACTTGAGATCAAAATATGACTTCTCTATATGAAAAGGAACACATCTGC 953
DB 541 TGGCAGTGCACAACTTGAGATCAAAATATGACTTCTCTATATGAAAAGGAACACATCTGC 600
QY 954 TGGTTAGAGAGTGCACAGCCCTGTGACCCAGAGAGTCTACACCCCTTCACTCTGCTGCT 1013
DB 601 TGGTTAGAGAGTGCACAGCCCTGTGACCCAGAGAGTCTACACCCCTTCACTCTGCTGCT 660
QY 1014 ATCTCTTCTCTCTGCTGCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1073
DB 661 ATCTCTTCTCTCTGCTGCTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
QY 1074 CTCTGGATAAAGAAAGAGTGGGATGCTTCACTGCTTTCGAACTTTCATGAAAAGAA 1133
DB 721 CTCTGGATAAAGAAAGAGTGGGATGCTTCACTGCTTTCGAACTTTCATGAAAAGAA 780
QY 1134 ATGTCAAAATAGCCAGGAGAGAGAACAGCTGCTCATTTATGATGTGTCAGTGGTGGCT 1193
DB 781 ATGTCAAAATAGCCAGGAGAGAGAACAGCTGCTCATTTATGATGTGTCAGTGGTGGCT 840
QY 1194 CTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1253
DB 841 CTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
QY 1254 TTGAAAAGGAATATGATGATGTCACAAATCAAGATGATTTTGTCTATCGTCAAAATATT 1313
DB 901 TTGAAAAGGAATATGATGATGTCACAAATCAAGATGATTTTGTCTATCGTCAAAATATT 960
QY 1314 GGATTTTCAACTCCATCTGTAATCCCATGCTATGCTGCTATGATGATGATGATGATGAT 1373
DB 961 GGCTTTTCAACTCCATCTGTAATCCCATGCTATGCTGCTATGATGATGATGATGATGAT 1020
QY 1374 AAAAATGTTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1433
DB 1021 AAGAATTTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
QY 1434 AGGCTGGAATTCAGGAATTAATGATGCGGAAGAAAGCAAGTTCCTTCAGAGAG 1493
DB 1081 AAGCCTGGAAATTCAGGAATTAATGATGCGGAAGAAAGCAAGTTCCTTCAGAGAG 1140
QY 1494 AATCCAGTGGAGAAACCAAGGAGAGATTCAGTGTGGCAACATTTGAAGTCAAATTTG 1553
DB 1141 CTTGAGTGGGAGAAACCAAGGAGAGATTCAGTGTGGCAACATTTGAAGTCAAATTTG 1200
QY 1554 TGTGAACACAGACAG 1613
DB 1201 TGTGAGCAGCAGGAG 1260
QY 1614 CTGGCTGAGAAATTTCTCTTTTACAGAGTGGGCAATTAATTAACAATATCTTCAATTA 1673

Db 1261 CTTTCTGAAACTTACTTTTCGGCAGTGGACATGAATGATATCCTCATAGCTAA 1320
 QY 1674 TGCCCTTCAGATTGTAACCCAAAGAGAAAATATTTTTCAGCAAAAGGTCAAATCTCTTTT 1733
 Db 1321 TATCATTTGTAT-----GGAAAGTATTTTAAAGCAAGGTGAGCACTATTTT 1368
 QY 1734 AATCTTAAAGTATGACAAGAGAAAACAAATCATGTTTCCATTTAAATAATGACAGAG 1793
 Db 1369 TTTAAATGACAAGAGAGAAAACAGACATGTTTCCATTTAAATGAAATATATATAAC 1428
 QY 1794 GCT 1796
 Db 1429 ACT 1431

RESULT 15
 ABK86293
 ID ABK86293 standard; cDNA; 1772 BP.
 AC ABK86293;
 DT 27-AUG-2002 (first entry)
 XX Mouse TGR346b cDNA.
 DE
 XX Mouse; TGR346b; gene; ss; G-protein coupled receptor; GPCR; TGR;
 KW TGR-associated disorder; signal transduction; renal failure; nephritis;
 KW hypothyroidism; hypogonadism; retinitis pigmentosa; growth disorder;
 KW diabetes insipidus; hyperprolactinaemia; thirst disturbance; appetite;
 KW sleep disturbance; temperature regulation; blood pressure; hypothalamus;
 KW circadian rhythm.
 KW
 XX Mus sp.
 OS
 XX
 PH Location/Qualifiers
 FT 1..1251
 FT /*tag= a
 FT /product= "Mouse TGR346b protein"
 XX
 WO200242458-A2.
 XX 30-MAY-2002.
 XX 21-NOV-2001; 2001WO-US43404.
 XX 22-NOV-2000; 2000US-252841P.
 PR 22-DEC-2000; 2000US-257636P.
 PR 12-JAN-2001; 2001US-261377P.
 PR 28-MAR-2001; 2001US-279554P.
 PR 29-MAR-2001; 2001US-280696P.
 XX (TULA-) TULARIK INC.
 XX PA
 XX Tian H, Zhao J, Chen J, Cutler G, An S, Dai X, Gupte JS;
 PI WPI; 2002-463633/49.
 XX P-PSDE; AAU97741.
 DR
 XX New isolated G-protein coupled receptor polypeptide, termed TGR, for
 PT diagnosis and treatment of diseases such as renal failure, nephritis,
 PT hypothyroidism, diabetes insipidus, and disturbances of thirst and
 FT sleep
 XX
 PS Claim 22; Page 78-79; 98pp; English.
 PS
 XX The invention relates to a G-protein coupled receptor polypeptide (GPCR),
 CC termed TGR, and its associated nucleic acid. The sequences of the
 CC invention are useful for identifying a compound that modulates signal
 CC transduction and for identifying a mammal having a TGR-associated
 CC disorder. The proteins and nucleic acids are useful in diagnosis and
 CC treatment of diseases or conditions such as renal failure, nephritis,
 CC hypothyroidism, hypogonadism, retinitis pigmentosa, growth disorders,

CC diabetes insipidus, hyperprolactinaemia and disturbances of thirst,
 CC sleep, temperature regulation, appetite, blood pressure or any other
 CC syndrome or disease associated with the hypothalamus. The sequences can
 CC be used in regulation of circadian rhythms, for use as genetic markers
 CC for the identification of mutations associated with diseases resulting
 CC from GPCR inactivation in particular cell types and for identification of
 CC modulators of GPCR signal transduction. This sequence represents cDNA
 CC encoding the mouse TGR346b polypeptide.
 XX
 SQ Sequence 1772 BP; 494 A; 390 C; 403 G; 485 T; 0 other;

Query Match 38.6%; Score 932; DB 24; Length 1772;
 Best Local Similarity 92.0%; Pred. No. 1.2e-138;
 Matches 1138; Conservative 0; Mismatches 235; Indels 15; Gaps 5;

QY 359 GGGCTTAAACATTACCCCGGAGAGTCTCTCGGCTGCTCGGGACACACCTGAGCG 418
 Db 3 GTCGTGGAAGCTTGACCGCGGAGCAGCTCTCGGGCTGCTCGGGCTGAGCGCG 62
 QY 419 GGAGCAGTTCATCGCTCTGTACCGGCTGCGACCGCTCGTCTACACCCAGAGCTGCCGG 478
 Db 63 CGCTCAGTTCATCGGCACTATGGCTGCGGCCACTGTGTCTCACCCGGCAGCTTCCGC 122
 QY 479 ACGGCCAAGCTGGCCCTCTGTCTACCGGCTGCTCACCGGCTGCTCATTTGCCCTGGCGCTTTGG 538
 Db 123 GCGCGCCAGGCTGGCCCTCTGTGTGTGTCGGCTGCGCATCTCTTTGCCCTGGCGCTTTGG 182
 QY 539 CAATGCTCTGGTCTTACGCTGTGACCCGACAGCCGATGCGGACCGTCCACACAT 598
 Db 183 CAACGCCCTGGTATCTATGTGTGACCCGACAGCCGATGCGGACCGTCCACACAT 242
 QY 599 CTTTATCTGCTCTTGGCGCTCAGTGACCTGCTCATCACCTTCTTGTGCATTCCTGCTCAC 658
 Db 243 CTTTATCTGCTCTTGGCGCTCAGTGACCTGCTCATCACCTTCTTGTGCATTCCTGCTCAC 302
 QY 659 CATGCTCCAGAAATTTCCGACAACTGGCTGGGGGGTCTTTTATTTGCAAGATGGTGCC 718
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and is derived by analysis of the total score distribution.

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3	1296	53.7	1296	6	AX665928	AX665928 Sequence
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16	309.2	12.8	227102	2	AC102844	AC102844 Mus muscu
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18	309	12.8	432	6	AX277395	AX277395 Sequence
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ALIGNMENTS

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LOCUS AX360197 1710 bp DNA linear PAT 13-FEB-2002
DEFINITION Sequence 3 from Patent WO0204518.
ACCESSION AX360197
VERSION AX360197.1 GI:18675761
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Bukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Bloomquist,B.T. and Zhelnin,L.
TITLE Human neuropeptide y-like g protein-coupled receptor
JOURNAL Patent: WO 0204518-A 3 17-JAN-2002;

Bayer Corporation (US)
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 DEFINITION Sequence 1 from Patent WO0204518.
 ACCESSION AX360195
 VERSION AX360195.1 GI:18675760
 KEYWORDS
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 ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
 1
 Bloomquist, B.T. and Zhelmin, L.
 Human neuropeptide y-like g protein-coupled receptor
 Patent: WO 0204518-A 1 17-JAN-2002;
 Bayer Corporation (US)
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Best Local Similarity 100.0%; Pred. No. 1.1e-254;
Matches 1296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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AUTHORS    Tian,H., Zhao,J., Chen,J.L., Cutler,G., An,S., Dai,K. and
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BASE COUNT      344 a   305 c   301 g   346 t
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Query Match      53.7%; Score 1296; DB 6; Length 1296;
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RESULT 4
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LOCUS
DEFINITION
Novel guanosine triphosphate-bound protein-coupled receptors and
genes encoding them, and their production and use.
ACCESSION
BD095744
VERSION
BD095744.1 GI:22641332
KEYWORDS
WO 0148189-A/2.
SOURCE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 1296)
AUTHORS
Matsumoto, S., Oda, T., Saito, Y., Noriyuki, Morikawa, Yoshida, K.,
Suwa, M. and Sugiyama, T.
TITLE
Novel guanosine triphosphate-bound protein-coupled receptors and
genes encoding them, and their production and use
JOURNAL
Patent: WO 0148189-A 2 05-JUL-2001;
HELIIX RESEARCH INSTITUTE, SHUNICHIRO MATSUMOTO, TAKAKI ODA, YOKO
SAITO, NORIYUKI MORIKAWA, KENJI YOSHIDA, MAKIKO SUWA, TOMOYASU
SUGIYAMA

COMMENT
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PN WO 0148189-A/2
PD 05-JUL-2001
PF 28-DEC-2000 WO 2000JP009409
PR 28-DEC-1999 JP 99P 375152, 31-MAR-2000 JP 00P 101339 PR
23-MAY-2000 JP 00P 155978
PI SHUNICHIRO MATSUMOTO, TAKAKI ODA, YOKO SAITO, NORIYUKI PI
MORIKAWA, KENJI YOSHIDA,
PI MAKIKO SUWA, TOMOYASU SUGIYAMA
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ACCESSION          BD012995.1 GI:22093184
VERSION            WO 0116316-A/1.
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                    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE           1. (bases 1 to 1293)
AUTHORS            Watanabe,T., Kikuchi,K. and Shintani,Y.
TITLE              Novel G protein coupled receptor protein and its DNA
JOURNAL            Patent: WO 0116316-A 1 08-MAR-2001;
                    TAKEDA CHEMICAL INDUSTRIES LTD, TAKUYA WATANABE, KUNIKO KIKUCHI,
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RESULT 6
BD014506
LOCUS
DEFINITION Novel G protein-coupled receptor protein and DNA thereof.
ACCESSION BD014506
VERSION BD014506.1 GI:22555289
KEYWORDS JP 2001136981-A/1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 1293)
Watanabe, T., Kikuchi, K. and Shintani, Y.
Novel G protein-coupled receptor protein and DNA thereof
Patent: JP 2001136981-A 1 22-MAY-2001;
TAKEDA CHEMICAL INDUSTRIES LTD
COMMENT OS Homo sapiens (human)
PN JP 2001136981-A/1
PD 22-MAY-2001
PF 24-AUG-2000 JP 2000253667
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QY 1369 TCAAAAAAATGTTTGTCTGCAGTTTGTATTGCATAGTAAATAAAACCTTCTCTCCAG 1428
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QY 1429 CACAAAGCATGGAATTCAGGAATTAACAATGATCGGAGAGAAAGAGCAAGTTTCCCTCA 1488
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QY      2329 TGCTAGATTGAATAAGAAAATAAATAATATCTTCTCTGTAAGAAAAAATTTTTTTCGA 2385
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RESULT 9
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DEFINITION    Homo sapiens, *** SEQUENCING IN PROGRESS ***, 8 unordered pieces.
AC005961
VERSION       AC005961.2 GI:21406543
KEYWORDS      HTG; HTGS PHASE1.
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE     1 (bases 1 to 155347)
AUTHORS       Evans, G.A., Athanasiou, M., Aguayo, P., Armstrong, D., Basit, M.,
               Buettner, J., Butler, C., Card, P., deSailboat, C., Dunn, J.,
               English, C., Ehrbridge, S., Garner, H.R., Gordon, M., Grant, O.,
               Hahner, L., Joslin, J., Lewis, E., Loo, H., Loo, K.N., Major, T.,
               McFarland, J., Newton, J., Osborne-Lawrence, S., Schageman, J.,
               Schultz, R.A., Stimson, S., Wagner, N., Waller, M. and Ward, T.
               HTGS Submission
TITLE         Direct Submission
JOURNAL
REFERENCE     2 (bases 1 to 155347)
AUTHORS       Evans, G.A., Athanasiou, M., Aguayo, P., Armstrong, D., Basit, M.,
               Buettner, J., Butler, C., Card, P., deSailboat, C., Dunn, J.,
               English, C., Ehrbridge, S., Garner, H.R., Gordon, M., Grant, O.,
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               Schultz, R.A., Stimson, S., Wagner, N., Waller, M. and Ward, T.
               Direct Submission
TITLE         Submitted (11-NOV-1998) Genome Science & Technology Center,
               University of Texas Southwestern Medical Center, 5323 Harry Hines
               Blvd., Dallas, TX 75235-8591, USA
COMMENT       On Jun 13, 2002 this sequence version replaced gi:3859648.
               * NOTE: This is a 'working draft' sequence. It currently
               * consists of 8 contigs. The true order of the pieces
               * is not known and their order in this sequence record is
               * arbitrary. Gaps between the contigs are represented as
               * runs of N, but the exact sizes of the gaps are unknown.
               * This record will be updated with the finished sequence
               * as soon as it is available and the accession number will
               * be preserved.
               * 1 4940: contig of 4940 bp in length
               * 4941 5040: gap of 100 bp
               * 5041 9845: contig of 4805 bp in length
               * 9846 9946: gap of 100 bp
               * 9946 13197: contig of 3252 bp in length
               * 13197 13297: gap of 100 bp
               * 13298 24220: contig of 10923 bp in length
               * 24220 24321: gap of 100 bp
               * 24321 37476: contig of 13156 bp in length
               * 37477 37576: gap of 100 bp
               * 37577 66711: contig of 29135 bp in length
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FEATURES             * 105937 155347: contig of 4941 bp in length.
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RESULT 10

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LOCUS AX549224 1368 bp DNA linear PAT 26-NOV-2002

DEFINITION Sequence 509 from Patent WO02061087.

ACCESSION AX549224

VERSION AX549224.1 GI:25813923

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1

AUTHORS Burmer, G.C., Roush, C.L. and Brown, J.P.

TITLE Antigenic peptides, such as for G protein-coupled receptors (GPCRs), antibodies thereto, and systems for identifying such antigenic peptides

JOURNAL Patent: WO 02061087-A 509 08-AUG-2002;

FEATURES

Location/Qualifiers

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Best Local Similarity 91.3%; Pred. No. 3.6e-210;

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Db 215 AGTTCTCTCGCTGCTGGGACACCAACCTGACCGGAGCAGTTTCATCGCTCTGTACC 274

Qy 442 GGCTGGACCGCTCGTTACACCCAGAGCTGCGGGAGCGGCCAAGCTGGCCCTGTGC 501

Db 275 GGCTGGACCGCTCGTTACACCCAGAGCTGCGGGAGCGGCCAAGCTGGCCCTGTGC 334

Qy 502 TCACCGGCTGCTCATCTTTCGCTGCGCTGCTTGGCAATGCTGCTGCTTCTACGTGG 561

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Qy 682 ACTGCTGGGGGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 741

Db 515 ACTGCTGGGGGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 574

Qy 742 TGACAGAAATCTCTATGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 801

Db 575 TGACAGAAATCTCTATGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 634

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RESULT 11

AF411117

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

cds.

AF411117

AF411117.1

GI:16566346

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AF411117 1368 bp mRNA linear PRI 01-NOV-2001

Homo sapiens G protein-coupled receptor (GPR103) mRNA, complete cds.

1
REFERENCE
AUTHORS Tian,H., Zhao,J., Chen,J.B., Cutler,G., An,S., Dai,K. and Gupte,J.S.
TITLE G-protein coupled receptors
JOURNAL Patent: WO 0242458-A 15 30-MAY-2002;
Tularik Inc. (US)
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QY 414 ACGGGAGAGTTATCGTCTGTATCCGCTGCGACCGCTCGTCTACACCCAGAGCTG 473
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QY 594 AACATCTTTATCTGCTCTTGGCGCTCAGTGACCTGCTATACACTTCTTTCGATCCG 653
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QY 954 TGCCTTAGAGTGGACAGCCCTGTGSCACCAAGAGATCTACACCACTTCTTCTCTTGTGTC 1013

Gupre,J.S.
 G-protein coupled receptors
 Patent: WO 0242458-A 17 30-MAY-2002;
 Tularik Inc. (US)
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 BASE COUNT 494 a 390 c 403 g 485 t
 ORIGIN

Query Match 38.6%; Score 932; DB 6; Length 1772;
 Best Local Similarity 82.0%; Pred. No. 3.4e-180;
 Matches 1138; Conservative 0; Mismatches 235; Indels 15; Gaps 5;

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 QY 479 ACGCCCAAGTGGCCCTGTGCTCACCGGCTGTCTATCTTGGCCCTGGGCTCTTTGG 538
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 QY 539 CAATGCTCTGTGTTCTACGTGGTACCGGACGAGCAGCCATGCGGCTGACCAACAT 598
 Db 183 CAACGCCCTGTGAGTCTATGTGGTACCGGACGAGCAGCCATGCGGCTGACCAACAT 242
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 Db 243 CTTTATCTGCTCTTGGGCTCAGTGACCTGTCTCATCCTTCTCTCTGCTATCCCGTCTAC 302
 QY 659 CATGCTCAGAACATTTCCGAACTGGCTGGGGGTGCTTTCAATTGCAAGATGGTGCC 718
 Db 303 CATGCTCAGAACGCTCTCGGACACCTGGCTGGGGGTGCTTTCAATTGCAAAATGGTGCC 362
 QY 719 ATTGTCCAGTCTACCGTGTGTGACAGAAATCTCTACTATGACTGCTGCTGTGGA 778
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 Db 543 TGTGAGCGGCTTGAGATTAAGTATGACTTCTATATGAAAGGAAACATCTGCTGCT 602
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QY 1019 CTTCTCTGCTCTTATGTGTGATGCTTATTTCTGTACAGTAAAAATTTGTTATGAACTTTG 1078
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 QY 1735 ATTCTTAA 1742
 Db 1372 ATTAAGAA 1379

RESULT 14
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 DEFINITION Sequence 17 from Patent WO03000893.
 ACCESSION AX657434
 VERSION AX657434.1 GI:29160173
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE 1
 AUTHORS Martinez R.M. and Sigurdsson G.T.
 TITLE Nucleic acids encoding G protein-coupled receptors
 JOURNAL Patent: WO 03000893-A 17 03-JAN-2003;
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BASE COUNT	241 a	231 c
ORIGIN	206 g	273 t
Query Match	32.7%	Score 790.8; DB 6; Length 951;
Best Local Similarity	89.0%	Pred. No. 2.3e-151;
Matches 924; Conservative 0; Mismatches 27; Indels 87; Gaps 3;		
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Qy	1254	TTTGAAAGGAATATGATGATGTCACAAATCAAGATGATTTTTCGATCTCGCAAAATTA 1313

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:

The RP11-11 human BAC library was made from the blood of one male donor, as described by Oseegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tatenno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at <http://www.chori.org> VECTOR: pBACe3.6

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is RP11-587P6. Actual start of this clone is at base position 73165 of RP11-587P6; actual end is at base position 170227 of RP11-364P2.

Data from AC093867 was used to finish this clone, AC093816.

Polymorphism has been identified between AC093867 and AC093816.

The sequence of AC055821 has been incorporated into AC093816.

FEATURES

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repeat_region	6907..6927 /rpt_family="AT_rich"
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repeat_region	7562..7651 /rpt_family="MaLR"
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repeat_region	8069..8089 /rpt_family="AT_rich"
repeat_region	8260..8422 /rpt_family="MER1_type"
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Best Local Similarity 99.9%; Pred. No. 6.6e-131;
Matches 694; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 29, 2003, 07:12:19 ; Search time 4992 Seconds
(without alignments)
11757.875 Million cell updates/sec

Title: US-10-070-241B-2

Perfect score: 2415

Sequence: 1 gccagaggccaggaccct.....aaaaaaaaaaaaaaagg 2415

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3: em_estin:*

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5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_htc:*

9: gb_est1:*

10: gb_est2:*

11: gb_htc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pln:*

20: em_gss_vit:*

21: em_gss_fun:*

22: em_gss_mam:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rtd:*

26: em_gss_dng:*

27: em_gss_vrl:*

28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	879.8	36.4	2864	11	AK048439	AK048439 Mus muscu
3	651.2	27.0	769	10	BG471265	BG471265 602512391
4	531.2	22.0	740	12	BT729969	BT729969 603350046

5	512.6	21.2	657	10	BB656182	BB656182
6	507.2	21.0	730	10	BG169612	BG169612 602312166
7	493	20.4	630	10	BB649191	BB649191 602312166
8	478.2	19.8	635	10	BB663258	BB663258 602312166
9	432.4	17.9	645	10	BB626475	BB626475 602312166
10	414.6	17.2	611	13	BU462231	BU462231 603775378
11	380.8	15.8	651	10	BB641290	BB641290 602312166
12	376.6	15.6	726	13	BU453865	BU453865 603770134
13	374.2	15.5	634	10	BB642180	BB642180 602312166
14	370.8	15.4	866	13	BQ735771	BQ735771 AGENCOURT
15	324	13.4	888	13	BU458649	BU458649 60367593
16	315.6	13.1	664	10	BB084541	BB084541 60367593
17	309	12.8	432	9	AI307658	AI307658 tb27a03.x
18	305.2	12.6	432	9	AI308124	AI308124 tb27a03.x
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20	302.6	12.5	642	9	AL651383	AL651383 AL651383
21	285	11.8	546	28	AZ454676	AZ454676 LM0258A18
22	252.6	10.5	609	9	AV760466	AV760466 AV760466
23	247.8	10.3	504	28	AQ215853	AQ215853 HS 3238 B
24	246.2	10.2	360	28	B91708	B91708 CIT-HSP-217
25	246.2	10.2	492	12	BM993628	BM993628 UI-H-DHO-
26	246.2	10.2	669	29	AG155696	AG155696 Pan trogl
27	246	10.2	876	28	AQ746417	AQ746417 HS 2278 A
28	245.8	10.2	672	29	AG084721	AG084721 Pan trogl
29	244.2	10.1	540	13	BUG17996	BUG17996 UI-H-DFO-
30	244.2	10.1	921	28	AQ738768	AQ738768 HS 5382 B
31	243.8	10.1	465	9	AI613280	AI613280 ty35e11.x
32	243.6	10.1	463	14	CA427664	CA427664 UI-H-DFO-
33	243.6	10.1	633	13	EX471308	EX471308 DKFZP686J
34	242.8	10.1	630	28	AQ628459	AQ628459 CITBI-E1-
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37	242.2	10.0	547	13	BU600474	BU600474 AGENCOURT
38	241.6	10.0	664	29	AG040130	AG040130 Pan trogl
39	241.4	10.0	660	29	AG113120	AG113120 Pan trogl
40	241.4	10.0	687	29	AG113667	AG113667 Pan trogl
41	241.2	10.0	342	9	AW276435	AW276435 xrl3d04.x
42	241.2	10.0	434	28	AQ483420	AQ483420 RPCI-11-2
43	241.2	10.0	924	28	AQ748907	AQ748907 HS 5574 A
44	241	10.0	471	28	AQ583262	AQ583262 RPCI-11-4
45	240.8	10.0	381	10	BG272215	BG272215 nah31d07.

ALIGNMENTS

RESULT 1	AK051723	1642 bp	mus musculus 12 days embryo spinal ganglion cDNA, RIKEN full-length enriched library, clone:DI30067L02 product:hypothetical Rhodopsin-like GPCR superfamily containing protein, full insert sequence.	linear	HTC 05-DEC-2002
LOCUS	AK051723				
DEFINITION	AK051723	GI:26342145			
ACCESSION	AK051723				
VERSION	AK051723.1				
KEYWORDS	HTC; CAP trapper.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
REFERENCE	AK051723				
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.				
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes				
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)				
MEDLINE	99279253				
PUBMED	10349636				
REFERENCE	AK051723				
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.				
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes				
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)				
MEDLINE	20499374				

Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL: <http://genome.gsc.riken.go.jp/>
URL: <http://fantom.gsc.riken.go.jp/>

FEATURES

source

Location/Qualifiers
1. 2864
/organism="Mus musculus"
/mol_type="mRNA"
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(InterPro|IPR000276, evidence: InterPro)
putative"

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IYTFILVFLPLGLLVLKIGYELKIKRIGDGLVLRTHIKENFKIARKKR
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BASE COUNT 839 a 609 c 602 g 814 t

Query Match 36.4%; Score 879.8; DB 11; Length 2864;
Best Local Similarity 82.5%; Pred. No. 1.4e-12;
Matches 1072; Conservative 0; Mismatches 212; Indels 15; Gaps 5;

QY 448 GACCGCTCGTACACCCACGAGCTGCGGACGCGCCAGCTGGCCCTCTGCTCACCG 507
DB 2 GGCACCTGGTCTCACCCCGCAGCTTCCCGCGCGCCAGCTGGCCCTCTGCTGTCG 61
QY 508 GCGTGTCTCATCTTCCGCTGCGCTCTTTGGCAATGCTCTGGTGTCTTACGTGGTACCC 567
DB 62 GCATGCTCATCTTGGCCCTGGCGCTCTTGGCAACGCGCTGGTGTCTATGTGTGACCC 121
QY 568 CCAGAGGCGCATGGCACCGTCCACACACTTTTATCTGCTCTGCGGCGCTCAGTGACC 627
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DB 182 TGCTCATCGTCTTCTTCTGCTATCCCGTCCAGTCCAGAACATTTCCGACAACTGGC 241
QY 698 TGGGGGTGCTTTCATTTGCAAGTGTGGCCATTTGCTTCCAGTCTACCGCTGTGTGACAG 747
DB 242 TGGGGGTGCTTTCATTTGCAAGTGTGGCCATTTGCTTCCAGTCTACCGCTGTGTGACAG 301
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QY 808 AAATGAAGTGGCAATACACCAACGAGGCTTTTCAATGCTAGGTGTGTCTGGCTGG 867
DB 362 AAATGAAGCGGAGTACCAATCAAGAGCTTTTCAATGCTAGGTGTGTCTGGCTGG 421
QY 868 TGGGAGTATGCTAGGATCACCATGCTGGCAGCTGACACACTTGCAGATCAATGACT 927
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QY 928 TCCTATATGAAGAAACACATCTGCTGTAGAGAGTGGACCGCCTGTGCACAGA 987

DB 482 TCCTATATGAAGAAACACATCTGCTGCTGGAAGTGGAGCGACGCCGCTGCACAGA 541
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DB 1251 TGAATTTGAGCAAGGTCATAATCTCTTTTAAATCTTAA 1289

RESULT 3

BG471265

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BG471265 769 bp mRNA linear EST 21-MAR-2001
602512391F1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:4634903 5',
mRNA sequence.
BG471265 GI:13403540
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 769)
NIH-MGC <http://mgc.nci.nih.gov/>
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov

FEATURES		source
Tissue Procurement: ATCC		
cDNA Library Preparation: Ling Hong/Rubin Laboratory		
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)		
DNA Sequencing by: Incyte Genomics, Inc.		
Clone distribution: WGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov		
Plate: LNCMI391 row: f column: 24		
High quality sequence stop: 765.		
Location/Qualifiers		
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/tissue_type="retinoblastoma"		
/lab_host="DH10B (phage-resistant)"		
/clone_lib="NIH_MGC_16"		
/note="Organ: eye; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH MGC Library."		
BASE COUNT	238 a	177 c 165 g 189 t
ORIGIN		
Query Match	27.0%; Score 651.2; DB 10; Length 769;	
Best Local Similarity	96.4%; Pred. No. 4e-07;	
Matches 740;	Conservative	0; Mismatches 20; Indels 8; Gaps 7;
QY	1564	CAGAGGAGAGAAAAAGCTCAACGACATCTTGTCTCTTTAGTGTCTGAATGGCTCAGA 1623
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QY	1684	ATTGTACCCAAAGAGAA--AATTATTTTGTGACCAAGCTCAATATCTTTTAATCTTAA 1742
Db	122	ATTGTACCCAAAGAGAA--AATTATTTTGTGACCAAGCTCAATATCTTTTAATCTTAA 181
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QY	1802	AAGTGCAGTGATGTTTACAACCAATNGATCACAATCATTTTAACANATTTCTGTGTTCCCT 1861
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QY	1862	CTCATTCCTCCACTGCTTCACATGTACTAGCCTTAAAAAGGACATGGAAGCCAGGACGG 1921
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QY	1922	TGGCTCATGCTGTAAATCCAGACACTTTGGGAGGCCCTAGACGGCGGATCACAGAGTCAG 1981
Db	362	TGGCTCATGCTGTAAATCCAGACACTTTGGGAGGCCCTAGACGGCGGATCACAGAGTCAG 421
QY	1982	GAGATCAAAACCATCTCTGGCTTAACACGGTGAAACCCCATCTCTGCTAAAAAATACAAAAT 2041
Db	422	GAGATCAAAACCATCTCTGGCTTAACACGGTGAAACCCCATCTCTGCTAAAAAATACAAAAT 481
QY	2042	TAGCCGGCGCTGGTGGCGGCACCTGTAGTCCAGCTACTTTGGAGGCTCAGGGCGAG-- 2100
Db	482	TAGCCGGCGCTGGTGGCGGCACCTGTAGTCCAGCTACTTTGGAGGCTCAGGGCGAG-- 541
QY	2101	AATGGTGTGAACCCGGAGGGCGGAGCTTGCAAGTATCCGAGATCATGCGCACTGCACCTCCA 2160
Db	542	AATGGTGTGAACCCGGAGGGCGGAGCTTGCAAGTATCCGAGATCATGCGCACTGCACCTCCA 601
QY	2161	-GCCTGGGCGAAAGAGCGAGACTCCCGCTCTCAAAAAAATTTTTTTTGAATAATTCGTAA 2219


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RESULT 6
BGL69612 730 bp mRNA linear EST 06-FEB-2001
LOCUS 60232126F1 NIH_MGC_89 Homo sapiens cDNA clone IMAGE:4424393 5',
mRNA sequence.
ACCESSION BGL69612
VERSION BGL69612.1 GI:12676315
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 730)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LRAM10168 row: c column: 18
High quality sequence stop: 726.
FEATURES
Location/Qualifiers
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Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.3 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
BASE COUNT 125 a 237 c 205 g 163 t
ORIGIN
Query Match 21.0%; Score 507.2; DB 10; Length 730;
Best Local Similarity 87.2%; Pred. No. 0.0006;
Matches 698; Conservative 0; Mismatches 3; Indels 99; Gaps 9;
Qy 1 GCCAGAGGCGCAGACCTAGCTGGCGCTCCAGACCCAGACCGTGGCGGCGCTCG 60
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Db 147 ATCGAGTCTCCAGTGTG-TTGGCTTCCGCTCTTTTATCGTGGTGTGATCCCTGAGCTG 205
Qy 181 CTCTCTCTTCCCGAACCTCCCGGGGTGCAGCTAGAGCCCTCCCGCGCGCTGATCTCCAG 240
Db 206 CTCTCTCTT----- 214
Qy 241 AGTAGAGGAGGAGGCGGCTCGGCTGCTCCCGAAGCCCTCGTCCGCGCAGATG 300
Db 215 -----CCCTCGCTGCGCGCAGATG 234
Qy 301 CGGATGCCAGCAGTAGCGGGGGTGGCCCGGCTCCCGGAGCGCACAGCAATGACGG 360
Db 235 CGGATGCCAGCAGTAGCGGGGGTGGCCCGGCTCCCGGAGCGCACAGCAATGACGG 294
Qy 361 CGTTTAACATTACCCGGAGCAGTTCTCTCGGTGTGCGGACCAACAACTGACGCGGG 420
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Qy 421 AGCAGTTCATCTGTGTACCGGCTGCGGCGCTCGTCTACACCCAGAGCTGCGGGAC 480
Db 354 AGCAGTTCATCTGTGTACCGGCTGCGGCGCTCGTCTACACCCAGAGCTGCGGGAC 412
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Db 711 AAGGCGACAGGAGGACTTTGTG 730

RESULT 7
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LOCUS BGL69191 RIKEN full-length enriched, 16 days embryo head Mus
DEFINITION musculus cDNA clone C130060K24 5', mRNA sequence.
ACCESSION BGL69191
VERSION BGL69191.1 GI:16483446
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 630)
AUTHORS Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.,
Hiramoto,K., Horii,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda,
M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M.,
Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki
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Query Match 20.4%; Score 493; DB 10; Length 630;
Best Local Similarity 86.5%; Pred. No. 0.0014;

JOURNAL
COMMENT

Unpublished
Contact: Yoshihide Hayashi
Laboratory for Genome Expl

Unpublished
Contact: Yoshihide Hayashi
Laboratory for Genome Expl

, size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."

BASE COUNT	144 a	153 c	134 g	180 t
ORIGIN				
Query Match	17.2%	Score 414.6;	DB 13;	Length 611;
Best Local Similarity	81.1%;	Pred. No. 0.074;		
Matches 494;	Conservative 0;	Mismatches 114;	Indels 1;	Gaps 1;

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QY 518 CTTTGGCCCTGGCGCTCTTTGGCAATGCTCTGGTGTCTTACGTGGTGACCGCAGCAAGGC 577
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QY 578 CATGGCAGCGGTACCAACATCTTATCTGCTCTCTGGCGCTAGTGACCTGTCTATCAC 637
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QY 938 AAGGAAACACATCTGCTGTAGAGAGTGGAACAGCCCTGTGCACAGAAGATCTACAC 997
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QY 1058 TAAATTTGGTTATGAACTTTTGGATATAAGAAAAGATTGGGGATGTTTCAGTGTCTCAAC 1117
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QY 1118 TATTCATGG 1126
Db 602 CATTCATGG 610
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RESULT 11	651 bp	mRNA	linear	EST 26-OCT-2001
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LOCUS				
DEFINITION	BB641290 RIKEN full-length enriched, 10 days neonate cortex Mus			
ACCESSION	musculus cDNA clone A830015G12 5', mRNA sequence.			
VERSION				
KEYWORDS	BB641290.1 GI:16476415			
SOURCE	EST.			
ORGANISM	Mus musculus (house mouse)			
REFERENCE	Mus musculus			
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Mus. 1 (bases 1 to 651)			
	Arakawa.T., Carninci.P., Fukuda.S., Furuno.M., Hanagaki.T., Hara.A.,			

, Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda,
 M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M.,
 Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki
 T., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H.,
 Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T.,
 Muramatsu,M. and Hayashizaki,Y.
 RIKEN Mouse ESTs (Arahawa,T., et al. 2001)
 Unpublished
 Contact: Yoshihide Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic
 Sciences Center (GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suehiro-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-res@gsc.riken.go.jp/
 URL:http://genome.gsc.riken.go.jp/
 Carninci, P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
 M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.,
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new
 genes. Genome Res. 10 (10), 1617-1630 (2000)
 wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
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 Hayashizaki,Y.
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 K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
 Hayashizaki,Y.
 Computational Analysis of Full-Length Mouse cDNAs Compared with
 Human genome Sequences. Mamm. Genome. 12, 673-677 (2001)
 Please visit our web site (<http://genome.gsc.riken.go.jp>) for
 further details.
 e mouse tissues.

FEATURES	Location/Qualifiers	131 a	193 c	151 g	172 t	4 others
source	1..551 /organism="Mus musculus" /mol_type="mRNA" /db_xref="taxon:10090" /clone="A830015g12" /tissue_type="cortex" /dev_stage="10 days neonate" /lab_host="PH108" /clone_lib="RIKEN full-length enriched, 10 days neonate cortex" /note="Site 1: Sall; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAGATCCAGAGCTCTTTTITTTTTTTTNN 3'], cDNA was prepared by using trihalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 20.0 and subtraction to Rot = 459.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGATTCGAGTTAATAATATACCCCCCCCCCC 3']. cDNA was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I."					

BASE COUNT
 131 a 193 c 151 g 172 t 4 others
 ORIGIN


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Matches 427; Conservative 0; Mismatches 77; Indels 0; Gaps 0;

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QY 773 TGTGGAAGGACACGAGGACTGTGCATCTTTTAAATGAAGTGGCATACCAACCG 832
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Db      |||
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Db      |||
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ACCESSION  BU453865
VERSION    BU453865.1
KEYWORDS   EST
SOURCE     Gallus gallus (chicken)
ORGANISM   Gallus gallus
REFERENCE  Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,
Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
TITLE      A Comprehensive Collection of Chicken cDNAs
JOURNAL    Curr. Biol. 12 (22), 1965-1969 (2002)
MEDLINE    22335534
PUBMED     12445392
COMMENT    Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology (UMIST)
)
PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.
Location/Qualifiers
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FEATURES
source

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/Note="Organ: ovary; Vector: pBluescript II KS(+); Site_1:
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constructed from 1 million independent clones. cDNA
synthesis was initiated using an oligo(dT) primer, using
methyated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA
was blunted, ligated to NotI adapters, digested with EcoRI
, size-selected, and cloned into the NotI and EcoRI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
(1996): 791, except that a significantly longer
reannealing hybridization was used."

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BASE COUNT      204 a 133 c 167 g 222 t
ORIGIN

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Query Match      15.6%; Score 376.6; DB 13; Length 726;
Best Local Similarity 74.5%; Pred. No. 0.44;
Matches 540; Conservative 0; Mismatches 179; Indels 6; Gaps 5;

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RESULT 15

BU458649

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

888 bp mRNA linear EST 29-NOV-2002

603367593F1 CSEQRN19 Gallus gallus cDNA clone cNEST269123 5', mRNA

sequence.

BU458649

BU458649.1 GI:25947960

EST

Gallus gallus (chicken)

Gallus gallus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Archosauria; Aves; Neognathae; Galliformes; Phasianidae;

Phasianinae; Gallus.

1 (bases 1 to 888)

Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,

Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.

A Comprehensive Collection of Chicken cDNAs

Curr. Biol. 12 (22), 1965-1969 (2002)

22335534

12445392

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Tel: 01612008930

Fax: 01612360409

Email: Simon.Hubbard@umist.ac.uk.

Location/Qualifiers

1..888

FEATURES

source

1..888

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Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.

FEATURES
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                EcoRI; Site_2: NotI; This normalized library was
                constructed from 1 million independent clones. cDNA
                synthesis was initiated using an oligo(dT) primer, using
                methylated C in the first strand synthesis reaction.
                Following this first strand reaction, double-stranded cDNA
                was blunted, ligated to NotI adapters, digested with EcoRI
                , size-selected, and cloned into the NotI and EcoRI
                compatible sites of a custom modified MCS of the
                pBluescript (KS-) vector. The library was normalized in 2
                rounds using conditions adapted from Soares et al., PNAS
                (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
                (1996): 791, except that a significantly longer
                reannealing hybridization was used."
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BASE COUNT
ORIGIN

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